



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 136079

TO: Bao-Qun Li
Location: REM-3D24/3C18
Art Unit: 1648
Monday, November 01, 2004

Case Serial Number: 10/089292

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Li,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

1999.09/30

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136079

STIC-Biotech/ChemLib

From: Li, Bao-Qun
Sent: Tuesday, October 26, 2004 7:36 AM
To: STIC-Biotech/ChemLib
Subject: FW: 10,089,292

-----Original Message-----

From: Li, Bao-Qun
Sent: Tuesday, October 26, 2004 7:31 AM
To: STIC-Biotech/ChemLib
Subject: 10,089,292

Please do the nucleic acid sequence homology and interference search against the amino acid sequence of SEQ ID NO:
2. Thanks.
Bao Qun Li
Art unit 1648.
Tel.20904.
REM, C18.

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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Protein Sequence Searches - 10/8/04

All of the sequence databases on the ABSS have been updated. A change has occurred in the protein databases.

- Two protein databases, SPTREMBL and SwissProt, are now produced as a single, merged database called UniProt.
- Results from UniProt have the file extension **.rup**.
- Sequences in UniProt are identified by the same ID that had been used in SPTREMBL or SwissProt.
- In instances where the database curators have determined that an SPTREMBL record and a SwissProt record represent the same sequence, the two records have been merged into one. Both IDs are present in the record. Any differences found between the two sequences are recorded in the FT (feature table) fields.

If you have any questions regarding these changes or your results, please contact any STIC searcher.

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions **.rnpm** and **.rnpn**

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions **.rapm** and **.rapn**

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 28, 2004, 10:18:59 ; Search time 2034 Seconds
(without alignments)
3815.960 Million cell updates/sec

Title: US-10-089-292A-2
Perfect score: 1095
Sequence: 1 QLFVSRPVSANGEPTVKLY.....SLGAGPVSISAVAVLAPPPR 213

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q/cgn2_1/USPRO_spool/US10089292/runat_27102004_153928_10167/app.query.fasta_1.391
-DB=EST -QWMT=fastcap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10089292 @CGN 1 1 2607 @runat_27102004_153928_10167 -NCPU=6 -ICPU=3
-NO MMAP -LARGESOURCY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hcc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsl1:*
9: gb_gsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	101	9.2	889	5 BQ681065	BQ681065 AGENCOURT
C 2	101	9.2	927	5 BUI74132	BUI74132 AGENCOURT
C 3	96.5	8.8	751	4 BM290684	BM290684 EST577218
C 4	96	8.8	935	5 BQ679041	BQ679041 AGENCOURT
C 5	95.5	8.7	665	6 CD901115	CD901115 G356.102N
C 6	95	8.7	791	6 CD575859	CD575859 UCRPT01.0
C 7	94	8.6	609	4 BM291795	BM291795 EST574337
C 8	94	8.6	904	6 CD792824	CD792824 EST664185
C 9	93	8.5	797	4 BM291070	BM291070 EST577604

10	92.5	8.4	553	4	BM676609	BM676609 UI-E-EJ0-
11	92.5	8.4	613	5	BQ684257	BQ684257 UI-CF-ENO
12	92.5	8.4	613	7	CN887504	CN887504 010512AAW
13	92.5	8.4	695	6	CB851742	CB851742 UI-CF-EN1
14	92.5	8.4	717	4	BM683536	BM683536 UI-E-E01-
15	92.5	8.4	909	4	BM801700	BM801700 AGENCOURT
16	92.5	8.4	1046	5	BX375570	BX375570 BX375570
C 17	92.5	8.4	1091	4	BG167780	BG167780 602339914
18	92	8.4	571	8	AW749973	AW749973 QV3-BT053
C 19	92	8.4	688	1	AL821981	AL821981 AL821981
C 20	92	8.4	1047	4	BG698844	BG698844 602703249
C 21	92	8.4	9183	9	AY400947	AY400947 Homo sapi
C 22	91.5	8.4	635	5	BUT73632	BUT73632 UI-B-CL1-
23	91.5	8.4	705	4	BG85589	BG85589 1024043C0
24	91	8.3	827	7	CK136482	CK136482 MM2_1_2_F
25	91	8.3	881	6	CD796381	CD796381 EST667742
26	90.5	8.3	9183	9	AY400948	AY400948 Pan trogl
27	90.5	8.3	687	4	BJ618104	BJ618104 BJ618104
C 28	90.5	8.3	700	7	CK863106	CK863106 34318 In
C 29	90.5	8.3	731	9	CC615969	CC615969 OGULV09TV
30	90	8.2	745	2	BF667907	BF667907 602122145
31	90	8.2	977	6	CA787406	CA787406 AGENCOURT
32	89.5	8.2	484	1	AL121209	AL121209 DKF2p762C
33	89.5	8.2	564	7	CN889248	CN889248 010604AAW
34	89.5	8.2	565	7	CN890116	CN890116 010617AAW
C 35	89.5	8.2	577	4	BM714229	BM714229 UI-E-EJ0-
36	89.5	8.2	590	7	CN947302	CN947302 020802AVB
37	89.5	8.2	605	6	CB660993	CB660993 OSJNED03E
38	89.5	8.2	619	7	CN908753	CN908753 030122ABL
39	89.5	8.2	648	7	CN889030	CN889030 010604AAW
40	89.5	8.2	649	7	CN908826	CN908826 030122ABL
41	89.5	8.2	652	7	CN881070	CN881070 010425AAS
42	89.5	8.2	776	7	CO389874	CO389874 AGENCOURT
43	89	8.1	468	1	AU190012	AU190012 AU190012
44	89	8.1	494	6	CD489573	CD489573 T25_C02 T
45	89	8.1	520	4	BG963333	BG963333 602827756

ALIGNMENTS

RESULT' 1
BQ681065/c
LOCUS BQ681065 889 bp mRNA linear EST 15-JUL-2002
DEFINITION AGENCOURT 8208181 NIH_MGC_112 Homo sapiens cdna clone IMAGE:6262741
5', mRNA sequence.
ACCESSION BQ681065
VERSION BQ681065.1 GI:21793744
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 889)
NIH-MGC <http://mgs.nci.nih.gov/>
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LUCM2425 row: i column: 14
High quality sequence stop: S75.
Location/Qualifiers
1. .889
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6262741"

[illegible]

```

Db 411 AGTGAGGACAGTCCACACCCGACCTGGACCCACCCACCCCTGGGTCTGTCCATCTCAGT 352
Qy 103 AspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaAraSerLeuAsp 122
Db 351 CCCGCGCTGAGCCTCTGGGCAAGCCACCTCTCTGAGCAGGCGAGGAGCGAAGAC 292
Qy 123 TrpThrLysValThrLeuAspGlyArgProLeuSer-----ThrIleGlnGlnTyrSer 140
Db 291 TGGGAGCAGCAGCAGCGGACGAGCAGCGCCCATGAGCCACCTCCACATCTCCAGATGGT 232
Qy 141 LysThrPhePheValLeuProLeu 148
Db 231 CAGAGTTACATGGTCACTCCCTG 208

RESULT 5
CD901115/c 665 bp mRNA linear EST 14-JUL-2003
LOCUS G356.102N03F010913 G356 Triticum aestivum cDNA clone G356102N03,
DEFINITION mRNA sequence.
ACCESSION CD901115
VERSION EST.
KEYWORDS Triticum aestivum (bread wheat)
SOURCE Triticum aestivum
ORGANISM Triticum aestivum
REFERENCE 1 (bases 1 to 665)
AUTHORS Genoplante, a major partnership french program in plant genomics
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'genoplante' (http://www.genoplante.com)
and http://genoplante-info.infobiogen.fr.

FEATURES
source
1..665
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="recital"
/db_xref="taxon:4565"
/clone="G356102N03"
/tissue_type="grain (356 degrees per day after
pollination)"
/clone_lib="G356"

ORIGIN
Alignment Scores:
Pred. No.: 3.18 Length: 665
Score: 95.50 Matches: 53
Percent Similarity: 35.14% Conservative: 25
Best Local Similarity: 23.87% Mismatches: 65
Query Match: 8.72% Indels: 79
Db: 6 Gaps: 10

US-10-089-292a-2 (1-213) x CD901115 (1-665)

Qy 2 LeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThr 21
Db 625 CTAATTACAGT---CCGCTCTCAGC-----CCAACGCTCTTTTGTGTTTCC 581
Qy 22 SerValGluAsnAlaGlnAspLysGlyIleAlaIleProHisAspLeuGly 41
Db 580 GGAACA----- 575
Qy 42 GluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrPro 61
Db 574 -----GATGAACAGCATCGTCGCTTCGCTCTCTCTGCT 542

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Qy 62 SerProLalaProSerArgProPheSerValLeuAraAsnAspValLeuTrpLeuSer 81
Db 541 GCCCTCTCCCTCGCTCTCCC----- 521
Qy 82 LeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrVal 101
Db 520 -----GAGCTCGCTCGGGTCCAGCGCGCGGTGAGGTGATGTG 482
Qy 102 SerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaAraSerLeu 121
Db 481 CTCCTCCACCATGACGCGCGAGCTGTCTCGCTCGGAGCGCGGCTCGCGGCATG 422
Qy 122 AspTrpThrLysValThrLeu-----AspGlyArgProLeuSerThrIleGlnGln 138
Db 421 TCATGGACCTCGATGGGAGGCGCATCCCGTCGGGCGAGTACCTCCGCGCAGTGCAGATG 362
Qy 139 TyrSerLysThrPhePheValLeu-----Pro-LeuArgGln 150
Db 361 AAGTAGTAGACTTGGCTCGCTCGTGGAGTAGGGATATCAGCGCCCGGAGGAGCGG 302
Qy 150 YLysLeuSerPheTrp---GluAlaGlyThrThrLysAlaGlyTyrPro-TyrAsnTyrA 169
Db 301 TAGATGGGTTTCTGGGGTCCACATGTCGAACCCGCGCTGTTCACTCCACCATC- 243
Qy 169 snThrThrAlaSerAspGlnLeuValGluAsnAlaAlaGlyHisArgValAlaIleS 189
Db 242 -----CAGCTTCTTGTCTCGCGCTGTAGAA---CACAGATA----- 210
Qy 189 erThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuA 209
Db 209 -----GTCTCTCTTGGAGAGGCGCGTGGCTCTTGGCCCGCAGTCCGAGTAGTGTG 161
Qy 209 la 209
Db 160 CT 159

RESULT 6
CD575859 791 bp mRNA linear EST 12-JUN-2003
LOCUS UCRPT01_02bb01_g3 Poncirus trifoliata CTV-challenged cDNA library -
DEFINITION AGI Poncirus trifoliata cDNA clone UCRPT01_02bb01, mRNA sequence.
ACCESSION CD575859
VERSION EST.
KEYWORDS Poncirus trifoliata
SOURCE Poncirus trifoliata
ORGANISM Poncirus trifoliata
REFERENCE 1 (bases 1 to 791)
AUTHORS Roose,M.L., Ye,X., Federici,C.F., Close,T.J., Fenton,R.D.,
Wanamaker,S., Collura,K., Feuerbacher,O., Kim,H.R., Kudrna,D.,
Wing,R. and Yu,Y.
TITLE Development of EST Resources and New Genetic Markers for California
JOURNAL Citrus - Poncirus trifoliata CTV-challenged phloem - AGI
COMMENT Unpublished (2003)
Contact: Mikeal Roose
Department of Botany & Plant Sciences, University of California
Riverside, CA, 92521-0124, USA
Tel: 9097874137
Fax: 9097874437
Email: mikeal.roose@ucr.edu
Seq primer: T3.
Location/Qualifiers
1..791
/organism="Poncirus trifoliata"
/mol_type="mRNA"
/cultivar="Pomeroy Op"
/db_xref="taxon:37690"
/clone="UCRPT01_02bb01"
/tissue_type="Phloem"
/dev_stage="10 - 30 cm shoots"
/lab_host="E. coli TJC121"

```

/clone_lib="Poncirus trifoliata CTV-challenged cdna library - Agi"
/note="vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI; Site 2: XhoI; Plants were grown in the greenhouse at University of California, Riverside. The scion was a open-pollinated (very probably selfed) seedling of Poncirus trifoliata cv Pomeroy that was selected as homozygous for the CTV resistance gene. The rootstock was sweet orange infected with citrus tristeza virus (CTV) isolate T514 over 1 year before sampling (CTV infects sweet orange, but not genotypes carrying the CTV resistance gene. Shoots 10-30 cm long were harvested in October 2000, and the green phloem (bark) was removed and frozen quickly in dry ice. Total RNA was extracted using Trizol reagent (Gibco). Poly(A) RNA was purified, a cDNA library was made, and 0.5 million primary lambda cDNA clones were in vivo excised to give a population of pBluescript SK(-) phagemids. All steps to this point were performed in the ML Roese lab at the University of California, Riverside by X. Ye. Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3730 at the Arizona Genomics Institute, University of Arizona (Collura, Feuerbacher, Kim, Kudrna, Wing, Yu). Chromatogram files were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Wanmaker) using the HarVest pipeline (<http://harvest.ucr.edu>) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."

ORIGIN

Alignment Scores:
Pred. No.: 4.59 Length: 791
Score: 95.00 Matches: 49
Percent Similarity: 37.50% Conservative: 23
Best Local Similarity: 25.52% Mismatches: 65
Query Match: 8.68% Indels: 56
DB: 6 Gaps: 9

US-10-089-292A-2 (1-213) x CD575859 (1-791)

Qy 3 PheTyrSerArgProValValSerAlaAsnGlyGlu-----ProThr 16
Db 146 TTTCCAAATCACCCTTGTTCACCTCAACGCAACAAATCGAAATCGTTTCCCTAAA 205
Qy 17 ValLysLeuTyrThrSerValGluAsnAlaGlnAspLysGlyLeAlaIleProHis 36
Db 206 CTGAATTTGACCCCTCAGTCTCAGCTCA-----CCCTCG 241
Qy 37 AspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGln 56
Db 242 GATCTGTCCGAGGATCCCTT----- 265
Qy 57 AspArgProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAsp 76
Db 266 ---TCCCATCTCCATCACCTCGCCGCAATCACTCAAGTATCGCTCCAAAGCAAGAA 322
Qy 77 ValLeuTrp-----LeuSerLeuThrAlaAlaGlu----- 86
Db 323 ACCCTGTACGGACTCTTCTCTCTCTTCTCTCCCACTTTCGCGAAATTTCCGGCGCTG 382
Qy 87 -----TyrAspGlnSerThrTyrGlySerThrGlyProValTyrValSerAspSer 104
Db 393 GCCGGTTACGATTCGTCTGTAGACATGAGACGCGCCCTCGCGGATTCCTCATGCT 442
Qy 105 ValThrLeuValAsn-----ValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAsp 122
Db 443 CTCGCTTCCCTTCACGCTTTCGCGCACGCGGACGCGGCAATTCCTCGGCTCCCTGAA 502
Qy 123 -----TrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 138
Db 123 ----- 141

Db 503 AGTTGCCCAACTGGGCTAAAGAGCCCTCGATCTGGGCCACACAGGGTCACTGT-CCC 561
Qy 139 Tyr-----SerLysThrPhePheValLeuProLeuArgGlyLys 151
Db 562 TATGATTGACTCCCCAGAGCCGCAAGAGCGGTGTCGTATTGCGGTTCCC----- 615
Qy 152 LeuSerPheTrpGluAlaGlyThrThrLysAlaGly 163
Db 616 ---GCCTTCTGAGTGGCGGATCCGCTCACACGGT 648

RESULT 7

BM291795 LOCUS BM291795 609 bp mRNA linear EST 01-JUL-2002
DEFINITION EST574337 AVSG Amblyomma variegatum cDNA clone AVABC55 5' end, mRNA sequence.

ACCESSION BM291795

VERSION BM291795.1 GI:21641762

KEYWORDS EST

SOURCE Amblyomma variegatum

ORGANISM Amblyomma variegatum
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Parasitiformes; Ixodida; Ixodidae; Amblyomma.

REFERENCE 1 (bases 1 to 609)
Nene, V., Lee, D., Quackenbush, J., Skilton, R., Mwaura, S.,

AUTHORS Gardner, M.J., and Bishop, R.

TITLE AVGI, an index of genes transcribed in the salivary glands of the ixodid tick Amblyomma variegatum

JOURNAL Int. J. Parasitol. 32 (12), 1447-1456 (2002)

MEDLINE 22281296

PUBMED 12392910

COMMENT Contact: Vish Nene

Parasite Genomics Group

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-610-5968

Fax: 301-838-0208

Email: nene@igr.org

Seq primer: M13 reverse.

Location/Qualifiers

source

1. 609

/organism="Amblyomma variegatum"

/mol_type="mRNA"

/db_xref="taxon:34610"

/clones="AVABC55"

/tissue type="Salivary glands"

/dev stage="Adult"

/lab_host="E.coli strain DH10B-Tona"

/clone_lib="AVSG"

/note="vector: pCMV-SPORT6.1; Salivary glands were

dissected on day five after initiation of feeding. Total

RNA was prepared using acid guanidinium

thiocyanate-phenol-chloroform extraction. The cDNA library

was custom prepared by Invitrogen Corporation. Briefly,

first strand cDNA was primed using oligo(dT) containing a

NotI site. Size fractionated double stranded cDNA was

ligated to EcoRV-NotI cleaved vector and electroporated

into E.coli."

ORIGIN

Alignment Scores:

Pred. No.: 4.17 Length: 609

Score: 94.00 Matches: 35

Percent Similarity: 41.01% Conservative: 22

Best Local Similarity: 25.18% Mismatches: 72

Query Match: 8.58% Indels: 10

DB: 4 Gaps: 3

US-10-089-292A-2 (1-213) x BM291795 (1-609)

Qy 8 ValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGln 27

Db 63 GTCACATGATGATACCGGTATACCGTACTTGGCGCAAAATAGCCTAATATCAAGTCT 122

```
QY 28 GlnAspLysGlyIleAlaIleProHisAspIleAspLeuGlyGluSerArgValValle 47
Db 123 GAAATCAGGTATACAGGCTTCTGTACAAATGACACCAAGAGCTCGACCGTTCGTCTG 182
QY 48 GlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArg 67
Db 183 GCTAAAGTACGGCTCTTTGGCAGAGAAGATCCCTTACTGACCGCCCTGTACACACTAGA 242
QY 68 -----ProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThr 83
Db 243 GATGAAGTCTACGAGTACATATCTTCAGGCGCCATGACATCAAGACCTTCGTGTGCC 302
QY 84 AlaAlaGluTyrAspGlnSerThrTyr-----GlySerSerThrGlyProValTyrVal 101
Db 303 GAGCCTCCGAAGCCCGAGTCAACTCTGCGCGAGGCGCTCACAAATGATCCTGCCATTGT 362
QY 102 SerAspSerValTrpLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeu 121
Db 363 CAACATTCAGCTACACCCATTGGTGTGGAGCAGGCTTTCTGCGCGCTGCG----- 413
QY 122 AspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
Db 414 ---TACAACCGAGCGACCTGCACCATATGCTCCAGTGGGTACTCTGCCGTCAATATCA 467

RESULT 8
CD792824 904 bp mRNA linear EST 01-JUL-2004
LOCUS EST664185 RAB Rhipicephalus appendiculatus cDNA clone RAB659 5'
DEFINITION end. mRNA sequence.
ACCESSION CD792824.1 GI:49548498
VERSION CD792824.1
KEYWORDS Rhipicephalus appendiculatus
SOURCE Rhipicephalus appendiculatus
ORGANISM Rhipicephalus appendiculatus
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Parasitiformes; Ixodidae; Ixodidae; Rhipicephalus.
REFERENCE Nene, V., Lee, D., Skilton, R., Mwaura, S., Quackenbush, J., Gardner, M.
AUTHORS 1 (bases 1 to 904)
TITLE An index of genes transcribed in the salivary glands of
JOURNAL Rhipicephalus appendiculatus
COMMENT Unpublished (2003)
Other ESTs: EST664184
Contact: Vishvanath Nene
Parasite Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-610-5968
Fax: 301-838-0208
Email: nene@tigr.org
Seq primer: M13 reverse.

FEATURES
source
1. 904
/organism="Rhipicephalus appendiculatus"
/mol_type="mRNA"
/strain="Muguga"
/db_xref="taxon:34631"
/clone="RAB659"
/dev_stage="Adult"
/lab_host="E. coli strain DH10B-Tona"
/clone_lib="RAB"
/notes="Organ: Salivary glands; Vector: pCMVSPORT6.0.ccdB;
Salivary glands were dissected on day four after
initiation of feeding. Total RNA was prepared using acid
guanidium thiocyanate-phenol-chloroform extraction. The
cDNA library was custom prepared by Invitrogen
Corporation. Briefly, first strand cDNA was primed using
oligo(dT) containing a NotI site. Size fractionated double
stranded cDNA was ligated to EcoRV-NotI cleaved vector and
electroporated into E.coli. Library RAB was made from
ticks infected with Theileria parva."
```

```
Alignment Scores:
Pred. No.: 7.15 Length: 904
Score: 94.00 Matches: 48
Percent Similarity: 43.17% Conservative: 31
Best Local Similarity: 26.23% Mismatches: 73
Query Match: 8.58% Indels: 32
DB: 6 Gaps: 8

US-10-089-292A-2 (1-213) x CD792824 (1-904)
QY 7 ProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerVal-GluAsnAl 26
Db 83 CCGTACTTTGAGCGCAGCAAAATAAGCCTAATATCAAGATCAGAGATTCGTATGAG---- 137
QY 26 aGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeuGlyGluSerArgValVa 46
Db 138 -----GGCATTTCTGTACACATTTGATACCAAGAGTCAACCGTCCG 178
QY 46 lIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSe 66
Db 179 TTTGGCTAAAGTGGCGTCTTTGGCAGCGAAGATCGCCCACTGATCGCGCAGTGGCACC 238
QY 66 rArg-----ProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerie 82
Db 239 TAGAGATGAAGTTTACGAGTACATCTCTCAGGCGCCATGACATCAAGATCTCAGAGT 298
QY 82 uThrAlaAlaGluTyrAspGlnSerThrTyr-----GlySerSerThrGlyProValTy 100
Db 299 GTCGGAGCGCTCTAAACCGCAGTCAACATTACCTGGTGGCCTTAACAAATGATCTCTAT 358
QY 100 rValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSe 120
Db 359 TGTTCAACATTCAGCTACT-----CCTGTTGGCACTGGAGCGCTTTTCTCGACCGCG 412
QY 120 rLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSe 140
Db 413 A-----TATGCGCAGCCAGCAGCTTCATATGTCCTCAGTGGGAGTTCACCGTCTTATTC 466
QY 140 rLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrTh 160
Db 467 TATGCGCTCC-TCAATATAC-----CTCGAGCGCTTCACAGCAGCAGCCACC 510
QY 160 rLysAla-----GlyTyrPro-----TyrAsnTyrAsnThrThrAlaSe 173
Db 511 CAAGTCTAGTGGATCCCAACAATCGGTTCCCACTCTGCGAGTACAACTCCTCGCAGCAGC 570
QY 173 rAspGln 175
Db 571 GGAAGAG 577

RESULT 9
BM291070 797 bp mRNA linear EST 01-JUL-2002
LOCUS EST577604 AVSG Amblyomma variegatum cDNA clone AVAAT96 5' end, mRNA
DEFINITION sequence.
ACCESSION BM291070
VERSION BM291070.1 GI:21641037
KEYWORDS EST.
SOURCE Amblyomma variegatum
ORGANISM Amblyomma variegatum
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Parasitiformes; Ixodidae; Ixodidae; Amblyomma.
REFERENCE 1 (bases 1 to 797)
AUTHORS Nene, V., Lee, D., Quackenbush, J., Skilton, R., Mwaura, S.,
Gardner, M.J. and Bishop, R.
TITLE AvGT, an index of genes transcribed in the salivary glands of the
JOURNAL ixodid tick Amblyomma variegatum
MEDLINE int. J. Parasitol. 32 (12), 1447-1456 (2002)
PUBMED 2281296
COMMENT 12392910
Contact: Vish Nene
Parasite Genomics Group
The Institute for Genomic Research
```

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-610-5968

Fax: 301-838-0208

Email: nene@tigr.org

Seq primer: M13 reverse.

Location/Qualifiers

FEATURES

source

1..797

/organism="Amblyomma variegatum"

/mol_type="mRNA"

/db_xref="taxon:34610"

/clone="AVAAT96"

/tissue_type="Salivary glands"

/dev_stage="Adult"

/lab_host="E.coli strain DH10B-Tona"

/clone_lib="AVSG"

/note="Vector: pCMV-SPORT6.1; Salivary glands were

dissected on day five after initiation of feeding. Total

RNA was prepared using acid guanidinium

thiocyanate-phenol-chloroform extraction. The cDNA library

was custom prepared by Invitrogen Corporation. Briefly,

first strand cDNA was primed using oligo(dT) containing a

NotI site. Size fractionated double stranded cDNA was

ligated to EcoRV-NotI cleaved vector and electroporated

into E.coli."

ORIGIN

Alignment Scores:

Pred. No.: 7.82 Length: 797
Score: 93.00 Matches: 56
Percent Similarity: 37.04% Conservative: 34
Best Local Similarity: 23.05% Mismatches: 105
Query Match: 8.49% Indels: 49
DB: 4 Gaps: 9

US-10-089-292A-2 (1-213) x BM291070 (1-797)

Qy 4 TyrSerArgProValSerAlaAsnGlyGluProThrValLysLeuTyThrSerVal 23
Db 82 TACCGGTATACCGTACTTGGCGAGCAAAATAGCCTATATCAAGTCTGAATCAGGTA 141
Qy 24 -GluAsnAlaGlnGlnAspLysGlyLeAlaIleProHisAspLeuGlyGluSe 43
Db 142 TGAA-----GGCATCTGTACACAATGTACCAAGATC 177
Qy 43 rArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerPr 63
Db 178 GACCGTTGCTCGGCTAAAGTACGGTCCTTTGGCACAGAGATCGCCCTACTGACCGGCC 237
Qy 63 oAlaProSerArg-----ProPheSerValLeuArgAlaAsnAspValLeuTr 79
Db 238 TGTAGCACCTAGAGATGAAGTCTACGAGTACATTATCTTCAGGGCCCATGACATCAAGA 297
Qy 79 pLeuSerLeuThrAlaAlaGluTyAspGlnSerThrTy-----GlySerSerThrGl 97
Db 298 CTTTGTGTGTCGAGAGCTCCGAGAGCCCGAGTCAACTGTGCCGAGGAGCCTCACAATGA 357
Qy 97 yProValTyValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaVa 117
Db 358 TCCTGCCATTGTCACATTACAGTACACCCATGGTCTGGAGCAGGCTTCTTCGCC 417
Qy 117 lAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIle-- 136
Db 418 TGG-----TACAACAGGAGCCCTGCACCATATGTCAGTGGGTACTCTGCC 465
Qy 137 -----GlnGlnTySerLysThrPhePheVal----- 145
Db 466 GTCATATTCAATGGCTCCACAGTACTCTTC-ACAACCTTCACAGCCACGACGAGCAAGCC 524
Qy 146 -----LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrLysAlaGl 163
Db 525 TAGTGGGTCCGACCAATC---AGTTCTCAGTCTGGAAGCACACACTCCACGACGCGGA 581
Qy 163 yTyProTyArgAsnTy-----AsnThrThrAl 172

Db 582 AGACCCCAACAATAGATGCTGGAGTACAGGTTTTCAGTCCCCCCTGAAACACAGT 641
Qy 172 aserAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgVal-----AlaIleSe 189
Db 642 CTCCTCGTGGTGGCTCTCAGCGCAGCCATGGGCGAGCAAGTTCTGCAGGACCTAGCAGG 701
Qy 189 rThrTyThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAl 209
Db 702 CAGCATGTCAGCAACATGGGCGAGCAGCATCACCAGCAGCATAGCCACAGCACCACGAG 761
Qy 209 aProPro 211
Db 762 CAGACCC 769

RESULT 10

BM676609

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

BM676609 553 bp mRNA linear EST 27-FEB-2002
UI-E-EJ0-ahq-h-20-0-UI.s2 UI-E-EJ0 Homo sapiens cDNA clone
UI-E-EJ0-ahq-h-20-0-UI 3', mRNA sequence.

BM676609

BM676609.1 GI:18986505

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 553)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

8889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).

Seq primer: M13 Forward

PolyA=yes.

FEATURES

source

1..553

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="UI-E-EJ0-ahq-h-20-0-UI"

/tissue_type="fetal eyes, lens, eye anterior segment,

optic nerve, retina, Retina Foveal and Macular, RPE and

Choroid"

/dev_stage="fetal and adult"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone_lib="UI-E-EJ0"

/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a

modified polylinker; Site 1: EcoR I; Site 2: Not I;

UI-E-EJ0 is a subtracted cDNA library constructed

according to Bonaldo, Lennon and Soares, Genome Research,

6:791-806, 1996. First strand cDNA synthesis was primed

with an oligo-dT primer containing a Not I site. Double

stranded cDNA was ligated to an EcoR I adaptor, digested

with Not I, and cloned directionally into pT7T3-Pac

vector. The oligonucleotide used to prime the synthesis of

first-strand cDNA contains a library tag sequence that is

located between the Not I site and the (G)18 tail. The

sequence tags for this library are: fetal eyes,

AGAAATCAAGA; lens, CGATTACGA; eye anterior segment, AATGCCGAT; optic nerve, CCATTAGTG; retina, CCGCG; Retina Foveal and Macular, GTC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
TAG_TISSUE=human optic nerve
TAG_LIB=UI-E-EJO
TAG_SEQ=CCATTAGTG

ORIGIN

Alignment Scores:
Pred. No.: 5.41 Length: 553
Score: 92.50 Matches: 30
Percent Similarity: 43.64% Conservatives: 18
Best Local Similarity: 27.27% Mismatches: 41
Query Match: 8.45% Indels: 21
DB: 4 Gaps: 4

US-10-089-292A-2 (1-213) x BM676609 (1-553)

QY 38 lleAspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHis----- 54
DB 204 CTGGATTGGGAGGTGGACAGGGGATCTTCAACCCCTACCATCTATCCAGGGGTC 263
QY 55 -----GluGlnAspArgProThrProSerProAlaProSerArgProPheSerValLeu 72
DB 264 ATGTGTCCAGCTGTTCAGAGCAGTCCCAATCTGTCTCCCATCTACCTCTGGGACATCTG 323
QY 73 ---ArgAlaAsnAspValLeuThrLeuSerLeuThrAlaAlaGluTyrAspGlnSerThr 91
DB 324 TACAGGATTCCTCAGTCTCTCTGG---GAACCTAACCCACCTGCTAGCCATCTAGCTTC 380
QY 92 TyrGlySerSer-----ThrGly 97
DB 381 TGGGCTCCACTGACGTGAGCAGACAGTCCACACCGACCTGGACCCCACTGGG 440
QY 98 ProValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaVal 117
DB 441 TCTGTCCATCTCAGTCCCGCTGAGCTCTGGGCAAGCCACCTCTTCTGAGCAGGCA 500
QY 118 AlaArgSerLeuAspTrpThrIysValThr 127
DB 501 GGCAGAGCGAGAGACTGGGAGCAGCAGACA 530

RESULT 11

BU684257 613 bp mRNA linear EST 07-OCT-2002
LOCUS UI-CF-ENO-aco-e-22-0-UI.s1 UI-CF-ENO Homo sapiens cDNA clone
DEFINITION UI-CF-ENO-aco-e-22-0-UI 3', mRNA sequence.

ACCESSION BU684257

VERSION BU684257.1 GI:23537029

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 613) Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene

discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT

Contact: McCray, PB

McCrack Lab

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA-res.

FEATURES

source

Location/Qualifiers
1..613
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-ENO-aco-e-22-0-UI"
/tissue_type="Primary Lung Cystic Fibrosis Epithelial Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-ENO"
/note="Organ: Lung; Vector: p7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-ENO is a cDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (d)18 tail. The sequence tag for this library is CTGCTCAGGT.
TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG_LIB=UI-CF-ENO
TAG_SEQ=CTGCTCAGGT

ORIGIN

Alignment Scores:

Pred. No.: 6.23 Length: 613
Score: 92.50 Matches: 30
Percent Similarity: 43.64% Conservatives: 18
Best Local Similarity: 27.27% Mismatches: 41
Query Match: 8.45% Indels: 21
DB: 5 Gaps: 4

US-10-089-292A-2 (1-213) x BU684257 (1-613)

QY 38 lleAspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHis----- 54
DB 203 CTGGATTGGGAGGTGGACAGGGGATCTTCAACCCCTACCATCTATCCAGGGGTC 262
QY 55 -----GluGlnAspArgProThrProSerProAlaProSerArgProPheSerValLeu 72
DB 263 ATGTGTCCAGCTGTTCAGAGCAGTCCCAATCTGTCTCCCATCTATCCCTGGGACATCTG 322
QY 73 ---ArgAlaAsnAspValLeuThrLeuSerLeuThrAlaAlaGluTyrAspGlnSerThr 91
DB 323 TACAGGATTCCTCAGTCTCTCTGG---GAACCTAACCCACCTGCTAGCCATCTAGCTTC 379
QY 92 TyrGlySerSer-----ThrGly 97
DB 380 TGGGCTCCACTGACGTGAGCAGACAGTCCACACCGACCTGGACCCCACTGGG 439
QY 98 ProValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaVal 117
DB 440 TCTGTCCATCTCAGTCCCGCTGAGCTCTGGGCAAGCCACCTCTTCTGAGCAGGCA 499
QY 118 AlaArgSerLeuAspTrpThrIysValThr 127
DB 500 TGCAGAGCGAGAGACTGGGAGCAGCAGACA 529

RESULT 12

CN887504

```

LOCUS               613 bp mRNA                      EST 04-JUN-2004
DEFINITION          010512AAWA002206HT (AAWA) Royal Gala 59 DAFB seeds Malus x
                    domesticA cDNA clone AAWA002206, mRNA sequence.
ACCESSION            CN887504
VERSION              CN887504
KEYWORDS             CN887504.1 GI:48273746
SOURCE               EST.
ORGANISM             Malus x domestica (cultivated apple)
                    Malus x domestica
                    Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
                    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                    rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
REFERENCE            1 (bases 1 to 613)
AUTHORS              Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Jansen, B.,
                    McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
                    HortResearch Apple EST Project
TITLE                Unpublished (2004)
JOURNAL              Contact: Gleave, A.
COMMENT              Sequencing Facility
                    The Horticulture and Food Research Institute of New Zealand Ltd
                    120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
                    Tel: 00 64 09 815 4200
                    Fax: 00 64 09 815 4201
                    Email: est@hortresearch.co.nz.
                    Location/Qualifiers
                        1..613
                        /organism="Malus x domestica"
                        /mol_type="mRNA"
                        /db_xref="taxon:3750"
                        /clone="AAWA002206"
                        /tissue_type="Seed"
                        /dev_stage="59 days after full bloom"
                        /clone_lib="(AAWA) Royal Gala 59 DAFB seeds"
                        /note="vector: pBluescript SK(-); Library sequenced by
                        Genesys Research & Development"
FEATURES             source

```

ORIGIN

Alignment Scores:

Pred. No.:	6.23	Length:	613
Score:	92.50	Matches:	42
Percent Similarity:	37.50%	Conservative:	21
Best Local Similarity:	25.00%	Mismatches:	54
Query Match:	8.45%	Indels:	51
DB:	7	Gaps:	6

US-10-089-292A-2 (1-213) x CN897504 (1-613)

QY	73	ArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGlu	-----	86
	:			:
Db	10	AAGAAAAAGATCTAGTCTGGTTTGCCACAGGCCGCAGATGTTGCAACTTTTATC	69	
QY	87	-----	-----	88
	:			:
Db	70	TATTTAGTGAACCTTCCCATGTTTGTACGTTCTTCCACATATCCCATGGTGTAGT	129	
QY	89	GlnSerThrTyrGlySerSerThrGlyProValTyrValSerAspSerValThrLeuVal	108	
	:			:
Db	130	GATTCAACTTATCCATCAACA	-----	153
QY	109	AsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThrLeu	128	
	:			:
Db	154	GACGTAAGGACAGGA	-----	198
QY	129	AspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuProLeu	148	
	:			:
Db	199	GAGGGT	-----	252
QY	149	ArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTrp	168	
	:			:
Db	253	ACAGGGCAATTAGTCCAGAGGATATGGCTCTAACAGAGAGCTGGTTCCACGTCCTTCATGCT	312	
QY	169	AsnThrThrAlaSerAspGlnLeuLeu	-----	185
	:			:
Db	313	CAAGATACATCTAGCCCTTCCATTATTTGATGATTTTGAAGAACTGGGAAGGAGAACTTGAC	372	
	:			:

Qy	186	-----ValIaIleSeRThrTyrrThrThrSerLeuGlyAlaGlyProVal	200
Db	373	TTCTCTACTCGTGTAGTTGCCCTTACATTTTATCTCGCGTCTCTGGAAGAGCCCTATC	432
Qy	201	SerIleSeRAlaValAlaValLeu	208
Db	433	ACTTTTGGTGAGATAGAAGTCCTT	456
RESULT	13		
CB851742			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
COMMENT			

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FEATURES
source
    Location/Qualifiers
    1. .695
       /organism="Homo sapiens"
       /mol_type="mRNA"
       /db_xref="taxon:9606"
       /clone="UI-CF-EN1-ael-a-16-0-UI"
       /tissue_type="Primary Lung Cystic Fibrosis Epithelial
       Cells"
       /dev_stage="Adult"
       /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
       /clone_lib="UI-CF-EN1"
       /notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
       modified polylinker; Site 1: EcoR I; Site 2: Not I;
       UI-CF-EN1 is a normalized cDNA library containing the
       following tissue(s): Primary Lung Cystic Fibrosis
       Epithelial Cells. The library was constructed according to
       Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
       1996. First strand cDNA synthesis was primed with an
       oligo-dT primer containing a Not I site. Double stranded
       cDNA was ligated to an EcoR I adaptor, digested with Not
       I, and cloned directionally into pT7T3-Pac vector. The
       oligonucleotide used to prime the synthesis of
       first-strand cDNA contains a library tag sequence that is
       located between the Not I site and the (dT)18 tail. The
       sequence tag for this library is CTGCTCAGGT.
       TAG SEQ=None found"

```

ORIGIN	Alignment Scores:	Length:
inc_bq-hmc found	7.39	695

Score: 92.50 Matches: 30
Percent Similarity: 43.64% Conservatives: 18
Best Local Similarity: 27.27% Mismatches: 41
Query Match: 8.45% Indels: 21
DB: 6 Gaps: 4

US-10-089-292A-2 (1-213) x CB851742 (1-695)

QY 38 lleAspLeuGlyGluSerArgValValleGlnAspTyrAspAsnGlnHis----- 54
Db 204 CTGGATTTGGGAGGTGGAGAGGGATCTTCAACCCCTACCATCTATCCAGGGCTC 263

QY 55 -----GluGlnAspArgProThrProSerProAlaProSerArgProPheSerValLeu 72
Db 264 ATGTGTCAGCTGTCCAGAGCAGTCCCAATCTGCTCCCATCTACCTCGGGACATCTCTG 323

QY 73 ---ArgAlaAspValLeuTyrPheSerLeuThrAlaAlaGluTyrAspGlnSerThr 91
Db 324 TACAGGATTCCTCAGTCTCTCTGG---GAACCTAACCCACCTGGTACCCATCTAGCTTC 380

QY 92 TyrGlySerSer-----ThrGly 97
Db 381 TGGGGCTCCACTGACAGCAGTCCACACCCAGCTGGACCCCTGGG 440

QY 98 ProValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaVal 117
Db 441 TCTGTCCATCTCAGTCCCGGCTGAGCTCTGGGCCAAGCCACTCTTCTTGAGCAGGCA 500

QY 118 AlaArgSerLeuAspTyrThrIlysValThr 127
Db 501 GGCAGAGCGAGAGACTGGGAGCAGCAGACA 530

RESULT 14
BM683536 717 bp mRNA linear EST 27-FEB-2002
LOCUS UI-E-EO1-ajb-h-05-0-UI.s1 UI-E-EO1 Homo sapiens cDNA clone
DEFINITION UI-E-EO1-ajb-h-05-0-UI.3', mRNA sequence.
VERSION BM683536
KEYWORDS EST.
SOURCE BM683536.1 GI:18993432
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 717)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Forward
POLYA=Yes.

FEATURES
source
1..717
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EO1-ajb-h-05-0-UI"
/tissue_type="fetal eye"

/dev stages="fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EO1"
/notes="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EO1 is a normalized cDNA library containing the
following tissue(s): fetal eye. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
CGCGTATACC. This library was created for the program, Gene
Discovery in the Visual System, supported by National Eye
Institute (NEI).
TAG TISSUE=human fetal eye
TAG_LIB=UI-E-EO1
TAG_SEQ=CGCGTATACC"

ORIGIN

Alignment Scores:
Pred. No.: 7.71 Length: 717
Score: 92.50 Matches: 30
Percent Similarity: 43.64% Conservatives: 18
Best Local Similarity: 27.27% Mismatches: 41
Query Match: 8.45% Indels: 21
DB: 6 Gaps: 4

US-10-089-292A-2 (1-213) x BM683536 (1-717)

QY 38 lleAspLeuGlyGluSerArgValValleGlnAspTyrAspAsnGlnHis----- 54
Db 204 CTGGATTTGGGAGGTGGAGAGGGATCTTCAACCCCTACCATCTATCCAGGGCTC 263

QY 55 -----GluGlnAspArgProThrProSerProAlaProSerArgProPheSerValLeu 72
Db 264 ATGTGTCAGCTGTCCAGAGCAGTCCCAATCTGCTCCCATCTACCTCGGGACATCTCTG 323

QY 73 ---ArgAlaAspValLeuTyrPheSerLeuThrAlaAlaGluTyrAspGlnSerThr 91
Db 324 TACAGGATTCCTCAGTCTCTCTGG---GAACCTAACCCACCTGGTACCCATCTAGCTTC 380

QY 92 TyrGlySerSer-----ThrGly 97
Db 381 TGGGGCTCCACTGACAGCAGTCCACACCCAGCTGGACCCCTGGG 440

QY 98 ProValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaVal 117
Db 441 TCTGTCCATCTCAGTCCCGGCTGAGCTCTGGGCCAAGCCACTCTTCTTGAGCAGGCA 500

QY 118 AlaArgSerLeuAspTyrThrIlysValThr 127
Db 501 GGCAGAGCGAGAGACTGGGAGCAGCAGACA 530

RESULT 15

BM801700 909 bp mRNA linear EST 05-MAR-2002
LOCUS AGENCOURT 6458620 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5573496
DEFINITION 5', mRNA sequence.
ACCESSION BM801700
VERSION BM801700.1 GI:19118523
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 909)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM12320 row: k column: 01
High quality sequence stop: 631.
Location/Qualifiers
1. .909
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5573496"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 88"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."

FEATURES
source

ORIGIN

Alignment Scores:	10.7	Length:	909
Pred. No.:	92.50	Matches:	30
Score:	43.64%	Conservative:	18
Best Local Similarity:	27.27%	Mismatches:	41
Query Match:	8.45%	Indels:	21
DB:	4	Gaps:	4

US-10-089-292A-2 (1-213) x BM801700 (1-909)

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Db	375	ATGTGTCCAGCTGTCCAGACAGGTCCCAATCTGCTCCCATCTACCTGGGACATCCTG	316
Qy	73	---ArgAlaAsnAspValIleuThrLeuSerLeuThrAlaAlaGluTyrAspGlnSerThr	91
Db	315	TACAGGATTCCTCAGTCTCTG---GAACCTAACCCACCTGGTACCCATCTAGCTTC	259
Qy	92	TyrGlySerSer-----ThrGly	97
Db	258	TGGGGCTCCATGACAGTGAGGACAGTCCACCCGACCTGGACCCACCCTGGG	199
Qy	98	ProValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaVal	117
Db	198	TCTGTCCATCTCAGTCCGGCTGAGCTCTGGGCAAGCCACCTCTTCTGAGCAGGCA	139
Qy	118	AlaArgSerLeuAspTyrThrLysValThr	127
Db	138	GGCAGAGCGAAAGACTGGGAGCAGCAGACA	109

Search completed: October 28, 2004, 11:53:42
Job time : 2044 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 28, 2004, 10:19:49 ; Search time 67 Seconds
(without alignments)
2259.672 Million cell updates/sec

Title: US-10-089-292A-2
Perfect score: 1095
Sequence: 1 QLFYSRPVWSANGSPTVKLY.....SLGAGPVSISAVAVLAPPPR 213

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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-NO MMAP -LARGESQ=0 -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1076	98.3	984	1	US-08-240-049B-7
3	1076	98.3	984	1	US-08-259-148A-7
4	1076	98.3	984	1	US-08-484-054-7
5	1076	98.3	984	2	US-07-876-941A-7
6	1076	98.3	984	3	US-08-542-634-5
7	1076	98.3	984	3	US-08-477-292-5
8	1076	98.3	984	4	US-07-870-985A-7
9	1076	98.3	984	5	PCT-US95-13703-5
10	1076	98.3	1311	1	US-08-259-148A-9
11	1076	98.3	1311	1	US-08-484-054-9
12	1076	98.3	1311	2	US-07-876-941A-9

13	1076	98.3	1311	4	US-07-870-985A-9	Sequence 9, Appli
14	1076	98.3	1647	3	US-08-542-634-3	Sequence 3, Appli
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16	1076	98.3	1647	5	PCT-US95-13703-3	Sequence 3, Appli
17	1076	98.3	1658	4	US-09-172-699-15	Sequence 15, Appli
18	1076	98.3	1686	4	US-09-172-699-19	Sequence 19, Appli
19	1076	98.3	1983	1	US-08-240-049B-1	Sequence 1, Appli
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29	1076	98.3	2094	1	US-08-484-054-1	Sequence 1, Appli
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31	1076	98.3	2094	4	US-07-870-985A-1	Sequence 1, Appli
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44	1043	95.3	981	1	US-08-259-148A-8	Sequence 8, Appli
45	1043	95.3	981	1	US-08-484-054-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-172-699-17
; Sequence 17, Application US/09172699A
; Patent No. 6514500
; GENERAL INFORMATION:
; APPLICANT: Anderson, David A.
; APPLICANT: Locarnini, Stephen A.
; APPLICANT: Torelli, Joseph
; APPLICANT: Hui, Zhuang
; APPLICANT: Li, Fan
; TITLE OF INVENTION: IMMUNOREACTIVE ANTIGENS OF HEPATITIS E VIRUS
; FILE REFERENCE: Davies Col. Cave
; CURRENT APPLICATION NUMBER: US/09/172.699A
; CURRENT FILING DATE: 1998-10-14
; EARLIER APPLICATION NUMBER: 08/617,927
; EARLIER FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 803
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(801)
US-09-172-699-17

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Pred. No.: 6.07e-122 Length: 803
Score: 1076.00 Matches: 210
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 4 Gaps: 0

US-10-089-292A-2 (1-213) x US-09-172-699-17 (1-803)

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QY 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
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QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTyrLeu 80
DB 181 CTTTCCCGAGCCCATCGGCCCTTTCTGCTCCGAGCTAATGATGTGCTTGGCTT 240
QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
DB 241 TCTCTCACCGCTGCGAGTATGACAGTCCACTTACGGCTCTTCGACCGGCCGAGTCTAT 300
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QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTyrGluAlaGlyThrThr 160
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QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
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QY 201 SerIleSerAlaValAlaValLeuAlaPro 210
DB 601 TCTATTCCGCGGTGCTGTTTATAGCCCC 630

RESULT 2

US-08-240-049B-7

Sequence 7, Application US/08240049B

Patent No. 5686239

GENERAL INFORMATION:

APPLICANT: Reyes, Gregory R.

APPLICANT: Tam, Albert W.

APPLICANT: Yarbrough, Patrice O.

TITLE OF INVENTION: Hepatitis E Virus Peptides and Methods

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESS: Genelabs Technologies, Inc.

STREET: 505 Penobscot Drive

CITY: Redwood City

STATE: CA

COUNTRY: USA

ZIP: 94063

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/240,049B

FILING DATE: 09-MAY-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Charles K. Sholtz

REGISTRATION NUMBER: 38,615

REFERENCE/DOCKET NUMBER: 4600-0093.35; G32P4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 984 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain) SG3

US-08-240-049B-7

Alignment Scores:

Pred. No.: 8.38e-122 Length: 984

Score: 1076.00 Matches: 210

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 98.26% Indels: 0

DB: 1 Gaps: 0

US-10-089-292A-2 (1-213) x US-08-240-049B-7 (1-984)

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QY 21 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 40
DB 241 ACATCTGTAGAGATGCTCAGCAGGATAAGGTAATTGCAATCCCGCATGACATTCACCTC 300
QY 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
DB 301 GGAGAATCTCGTGTGTTTATTTCAGGATTAATGATACCAACATGAACAAGATCGGCCGAG 360
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DB 361 CCTTCTCCAGCCCCATCGGCCCTTCTCTGCTTCGAGTAATGATGCTTTGGCTC 420
QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
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QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
DB 481 GTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGCGCGAGCGGCTTGCCTCGGTG 540
QY 121 LeuAspTyrThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
DB 541 CTCGATTGGACCAAGGTACACTTTCAGCGTGCCTCCCTCTCCACCATCCAGCAGTCTG 600
QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTyrGluAlaGlyThrThr 160
DB 601 AAGACCTTCTTTGCTCTGCGCTCCGCGGTAAGCTCTCTTTCTGGGAGCGCAGCAACT 660
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DB 661 AAAGCGGGTACCTTTAATTAATTAACACCACTGTAGCAGCAACTGCTGCTCGAGAA 720
QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
DB 721 GCCCGCGGACACCGGTCGCTATTTCACCTTACACCACTAGCTGGGTGCTGCTCCGTC 780
QY 201 SerIleSerAlaValAlaValLeuAlaPro 210
DB 781 TCCATTCTCGGTTGCGGCTTTTAGCCCC 810

RESULT 3

US-08-259-148A-7

Sequence 7, Application US/08259148A
Patent No. 5741490
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R.
APPLICANT: Bradley, Daniel W.
APPLICANT: Twu, Jr-Shin
APPLICANT: Purdy, Michael A.
APPLICANT: Tam, Albert W.
APPLICANT: Krawczynski, Krzysztof Z.
APPLICANT: Yarbough, Patrice D.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,148A
FILING DATE: 13-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUN-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0093.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 984 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SG3, BURMA, FIGURE 7
US-08-259-148A-7

Alignment Scores:
Pred. No.: 8,38e-122
Score: 1076.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 98.26%
DB: 1

Length: 984
Matches: 210
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-089-292A-2 (1-213) x US-08-259-148A-7 (1-984)
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Qy 21 ThrSerValGluAsnAlaGlnGlnAspLysGlyLeuAlaIleProHisAspLeu 40
Db 241 ACATCTGTAGAGTAAGTCTCAGCAGGATAAGGTATTGCAATCCCGCATGACATTGACCTC 300
Qy 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
Db 301 GGAGAACTCTGTGGTTATTACAGATTATGATACCAACATGACACAGATCGCGCGAGC 360
Qy 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 80
Db 361 CTTTCTCCAGCCCATCGCGCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Qy 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
Db 421 TCTCTCACCCTGCGGAGTATGACCAAGTCCACTTATGGCTCTTCGACTGGCCCACTTAT 480
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Db 541 CTCGATTGGACCAAGTTCACACTTTCGCGTCCCGCTCTCCACCATCCAGCAGTACTCG 600
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Db 601 AAGACCTTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
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Db 661 AAAGCGGGTACCTTAT 720
Qy 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
Db 721 GCCCGCGGCGACCGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Qy 201 SerLeuSerAlaValAlaValLeuAlaPro 210
Db 781 TCCATTTCTGCGGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTC 810

RESULT 4
US-08-484-054-7
Sequence 7, Application US/08484054
Patent No. 5770689
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R.
APPLICANT: Bradley, Daniel W.
APPLICANT: Twu, Jr-Shin
APPLICANT: Purdy, Michael A.
APPLICANT: Tam, Albert W.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,054

aa against omo

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Qy	121	LeuAspTprThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlySer	140
Db	541	CTCGATTGGACCAAGGTCACACTTGAAGGTCGCGCCCTCTCCACCATCCAGCAGTACTCG	600
Qy	141	LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTprGluAlaGlyThrThr	160
Db	601	AAGACCTTCTTTGTCCTCGCGCTCCGCGGTAAAGCTCTCTTTCTGGAGGAGGACGACAACT	660
Qy	161	LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuValGluAsn	180
Db	661	AAAGCGGGGTACCTTATAATTATAACACCACTGTAGCGACCAACTGCTTGTGAGAAAT	720
Qy	181	AlaAlaGlyHisArgValAlaIleSerThrThrThrSerLeuGlyAlaGlyProVal	200
Db	721	GCGCGCGGGCACCGGGTGCCTATTATTCACCTTACACCACTAGCTGGGTGGTGGTCCGTC	780
Qy	201	SerIleSerAlaValAlaValLeuAlaPro	210
Db	781	TCATTTCTGCGGTTCGCGTTTTCGCGCC	810
<p>RESULT 5</p> <p>US-07-876-941A-7</p> <p>Sequence 7, Application US/07876941A</p> <p>Patent No. 5885768</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Reyes, Gregory R.</p> <p>APPLICANT: Bradley, Daniel W.</p> <p>APPLICANT: Tam, Albert W.</p> <p>APPLICANT: Mitchell, Carl</p> <p>TITLE OF INVENTION: Hepatitis E Virus Peptide Antigen and</p> <p>TITLE OF INVENTION: Antibodies</p> <p>NUMBER OF SEQUENCES: 76</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: Dehlinger & Associates</p> <p>STREET: 350 Cambridge Avenue, Suite 250</p> <p>CITY: Palo Alto</p> <p>STATE: CA</p> <p>COUNTRY: USA</p> <p>ZIP: 94306</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: Patentin Release #1.0, Version #1.25</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/07/876,941A</p> <p>FILING DATE: 01-MAY-1992</p> <p>CLASSIFICATION: 435</p> <p>Prior APPLICATION DATA:</p> <p>APPLICATION NUMBER: US 822,335</p> <p>FILING DATE: 17-JAN-1992</p> <p>Prior APPLICATION DATA:</p> <p>APPLICATION NUMBER: US 505,888</p> <p>FILING DATE: 05-APRIL-1990</p> <p>Prior APPLICATION DATA:</p> <p>APPLICATION NUMBER: US 420,921</p> <p>FILING DATE: 13-OCTOBER-1989</p> <p>Prior APPLICATION DATA:</p> <p>APPLICATION NUMBER: US 367,486</p> <p>FILING DATE: 16-JUNE-1989</p> <p>Prior APPLICATION DATA:</p> <p>APPLICATION NUMBER: US 336,672</p> <p>FILING DATE: 11-APRIL-1989</p> <p>Prior APPLICATION DATA:</p> <p>APPLICATION NUMBER: US 208,997</p> <p>FILING DATE: 17-JUNE-1988</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Sholtz, Charles K.</p> <p>REGISTRATION NUMBER: 38,615</p> <p>REFERENCE/DOCKET NUMBER: 4600-0093.33</p>			

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 984 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SG3, BURMA, FIGURE 7
US-07-876-941A-7

Alignment Scores:
Pred. No.: 8,38e-122 Length: 984
Score: 1076.00 Matches: 210
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 2 Gaps: 0

US-10-089-292A-2 (1-213) x US-07-876-941A-7 (1-984)

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Qy 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValIysLeuTyr 20
Db 181 CAGCTGTTCTACTCCCGTCCCGTCTCTCAGCAATGGCGAGCCGACTGTTAAGTTGAT 240
Qy 21 ThrSerValGluAsnAlaGlnAspIysGlyIleAlaIleProHisAspIleAspLeu 40
Db 241 ACATCTGTAGAGATGCTCAGCAGGATAGGTTATTCACATCCCGCATGACATTGACCTC 300
Qy 41 GlyGluSerArgValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
Db 301 GGAGAAATCTCGTGTGGTTATTTCAGGATTTATGTAACCAACATGAACAAGATCGGCCGACG 360
Qy 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTyrPleu 80
Db 361 CCTTCTCCAGCCCATCGCGCCCTTCTCTGCTCTTCGAGCTAATGATGCTTTGGCTC 420
Qy 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
Db 421 TCTCTCACCGTCCGAGTATGACAGTCCATTTATGCTCTTCGACTGGCCCAAGTTTAT 480
Qy 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
Db 481 GTTCTGACTCTGTGACCTTGGTTAATGTTGGACCGCGCGCGAGCGCGTGGCCGGTTCG 540
Qy 121 LeuAspThrThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
Db 541 CTCGATTGGACCAAGTCCACACTTGACGGTCCGCCCTCTCCACCATCCAGCAGTACTCG 600
Qy 141 LysThrPhePheValLeuProLeuArgGlyIysLeuSerPheTyrGluAlaGlyThrThr 160
Db 601 AAGACCTTCTTTGTCTCCCGCTCCCGGTAGCTCTCTTTCTGGAGCGAGGACAACT 660
Qy 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuValGluAsn 180
Db 661 AAAGCCGGTACCTTATATATATATACACCACTGCTAGCACCACACTGCTTGTGAGAAAT 720
Qy 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
Db 721 GCCCGCGGCGCCCGGTTCGCTATTTCCACTTACACCCTAGCCCTGGGTGCTGGTCCCGTC 780
Qy 201 SerIleSerAlaValAlaValLeuAlaPro 210
Db 781 TCCATTTCTGCGGTTCGCGGTTTTAGCCCCC 810
```

RESULT 6

US-08-542-634-5

; Sequence 5, Application US/08542634

; Patent No. 6214970

GENERAL INFORMATION:
APPLICANT: Fuerst, Thomas R.
APPLICANT: McAttee, C. Patrick
APPLICANT: Yarbrough, Patrice O.
APPLICANT: Zhang, Yifan
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542,634
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 984 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain) SG3
INDIVIDUAL ISOLATE: region
US-08-542-634-5

Alignment Scores:
Pred. No.: 8,38e-122 Length: 984
Score: 1076.00 Matches: 210
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 3 Gaps: 0

US-10-089-292A-2 (1-213) x US-08-542-634-5 (1-984)

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Qy 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValIysLeuTyr 20
Db 181 CAGCTGTTCTACTCCCGTCCCGTCTCTCAGCAATGGCGAGCCGACTGTTAAGTTGAT 240
Qy 21 ThrSerValGluAsnAlaGlnAspIysGlyIleAlaIleProHisAspIleAspLeu 40
Db 241 ACATCTGTAGAGATGCTCAGCAGGATAGGTTATTCACATCCCGCATGACATTGACCTC 300
Qy 41 GlyGluSerArgValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
Db 301 GGAGAAATCTCGTGTGGTTATTTCAGGATTTATGTAACCAACATGAACAAGATCGGCCGACG 360
Qy 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTyrPleu 80
Db 361 CCTTCTCCAGCCCATCGCGCCCTTCTCTGCTCTTCGAGCTAATGATGCTTTGGCTC 420
Qy 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
Db 421 TCTCTCACCGTCCGAGTATGACAGTCCATTTATGCTCTTCGACTGGCCCAAGTTTAT 480
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QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
Db 481 GTTCTGACTCTGTGACCTTGTGTAATGTGAGCCGGCGGCGAGCCGTTGCCCGGTCG 540
QY 121 LeuAspThrThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
Db 541 CTCGATTGACCAAGGTACACTTACGCTGCGCCCTCTCCACCATCCAGCAGTACTCG 600
QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 160
Db 601 AAGACCTCTTTGTCTGCTGCGCTCCGGTAAAGCTCTCTTTCTGGAGGAGGACCAACT 660
QY 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuValGluAsn 180
Db 661 AAAGCCGGGTACCTTATAATTATAACACCACTGCTAGCACCACCACTGCTTGTGAGAA 720
QY 181 AlaAlaGlyHisArgValAlaIleSerThrThrThrThrSerLeuGlyAlaGlyProVal 200
Db 721 GCCGCGGGGACCGGGTCCGCTATTTCCTTACACCACTAGCCTGGGTGCTGCTCCCGTC 780
QY 201 SerIleSerAlaValAlaValLeuAlaPro 210
Db 781 TCCATTCTGCGGTTGCCGTTTTCAGCCCC 810

RESULT 7

US-08-477-292-5
; Sequence 5, Application US/08477292
; Patent No. 6291641
; GENERAL INFORMATION:
; APPLICANT: Fuerst, Thomas
; APPLICANT: McAtee, Patrick
; APPLICANT: Yarbough, Patrice
; APPLICANT: Zhang, Yifan
; TITLE OF INVENTION: Hepatitis E Virus Antigens and Methods
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESS: Cathleen M. Desjardins, M.D.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: US
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,292
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,952
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, Allan A
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: G32P5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)369-9500
; TELEFAX: (415)368-0709
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 984 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain) SG3
; INDIVIDUAL ISOLATE: region
; US-08-477-292-5

Alignment Scores:

Pred. No.: 8,38e-122 Length: 984
Score: 1076.00 Matches: 210
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 3 Gaps: 0

US-10-089-292A-2 (1-213) X US-08-477-292-5 (1-984)

QY 1 GlnLeuPheTyrSerArgProValValSerAlaGlnGlyGluProThrValLysLeuTyr 20
Db 181 CAGCTGTTCTACTCCGCTCCGCTTCTCTCAGCAATGGCGAGCCGACTGTTAAGTTGTAT 240
QY 21 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 40
Db 241 ACATCTGTAGAGATGCTCAGCAGGATAGGGTATTGCAATCCCCCATGACATTGACCTC 300
QY 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
Db 301 GGAGAACTCTCGTGTGTTATTTCAGGATTATGATACCAACATGAACAAGATCGGCCGAG 360
QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 80
Db 361 CTTCTCCAGGCCCATCGGCCCTTCTCTGTCTTCGAGCTTAATGATGTCTTGGCTC 420
QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
Db 421 TCTCTCACCGCTGCCGAGTATGACCACTTATGCTCTTCGACTGGCCCGAGTTTAT 480
QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
Db 481 GTTCTGACTCTGTGACCTTGGTTAATGTTCGACCGCGCGCGAGCGCTTCCCGGTCG 540
QY 121 LeuAspThrThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
Db 541 CTCGATTGCGACCAAGGTACACTTTCACCGTCCGCCCTCTCCACCATCCAGCAGTACTCG 600
QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 160
Db 601 AAGACCTCTTGTCTGCTCCGCTCCGCGTAAAGCTCTCTTCTGGAGGAGGACCAACT 660
QY 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuValGluAsn 180
Db 661 AAAGCCGGGTACCTTATAATTATAACACCACTGCTAGCACCACCAACTGCTTGTGAGA 720
QY 181 AlaAlaGlyHisArgValAlaIleSerThrThrThrThrSerLeuGlyAlaGlyProVal 200
Db 721 GCCGCGGGGACCGGGTCCGCTATTTCCTTACACCACTAGCCTGGGTGCTGCTCCCGTC 780
QY 201 SerIleSerAlaValAlaValLeuAlaPro 210
Db 781 TCCATTCTGCGGTTGCCGTTTTCAGCCCC 810

RESULT 8

US-07-870-985A-7
; Sequence 7, Application US/07870985A
; Patent No. 6455492
; GENERAL INFORMATION:
; APPLICANT: Reyes, Gregory R.
; APPLICANT: Bradley, Daniel W.
; APPLICANT: Twu, Jr-Shin
; APPLICANT: Purdy, Michael A.
; APPLICANT: Tam, Albert W.
; APPLICANT: Krawczynski, Krzysztof Z.
; TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA

COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 20-APRIL-1992
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 822,335
 FILING DATE: 17-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 505,888
 FILING DATE: 05-APRIL-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 420,921
 FILING DATE: 13-OCTOBER-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 367,486
 FILING DATE: 16-JUNE-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 336,672
 FILING DATE: 11-APRIL-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 208,997
 FILING DATE: 17-JUNE-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE/DOCKET NUMBER: 4600-0093.30
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 984 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: SG3, BURMA, FIGURE 7
 US-07-870-985A-7

Alignment Scores:
 Pred. No.: 8,386-122 Length: 984
 Score: 1076.00 Matches: 210
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.26% Indels: 0
 DB: 4 Gaps: 0

US-10-089-292A-2 (1-213) x US-07-870-985A-7 (1-984)

Qy 1 GlnLeuPheTyrSerArgProValValSerAlaGlnGlyGluProThrValIysLeuTyr 20
 Db 181 CAGCTGTTCTACTCCCGCCGGTGTCTCAGCAATGGCGAGCCGACTGTTAAGTTGAT 240
 Qy 21 ThrSerValGluAsnAlaGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 40
 Db 241 ACATCTGTAGAGATGCTCAGCAGGATAGGGTATTGCATCCCGCATGACATTGACCTC 300
 Qy 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
 Db 301 GGAGAATCTCGTGGTTATTTCAGGATTATGATACCAACATGAACAAGATCGGCCGACG 360
 Qy 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTyrLeu 80
 Db 361 CCTTCTCCAGCCCATCGCCCTTTCTCTGCTTCGAGCTAATGATGCTTTGGCTC 420

Qy 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
 Db 421 TCTCTCACCGCTGCCGAGTATGACAGTCCACTTATGGCTCTTCGACTGGCCAGTTTAT 480
 Qy 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
 Db 481 GTTTCTGACTCTGTGACCTTGGTTAATGTTCCGACCGCGCGAGCGCTTGGCCGGTCG 540
 Qy 121 LeuAspTyrThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
 Db 541 CTCGATTGGACCAAGGTACACTTTCGCGTCCCGCTCTCCACCATCCAGCAGTACTCG 600
 Qy 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTyrGluAlaGlyThrThr 160
 Db 601 AAGACCTTCTTTGTCTCTGCCGCTCCGCGGTAAAGCTCTCTTTCTGGGAGGCAGCAACT 660
 Qy 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuValGluLeu 180
 Db 661 AAGCCGGGTACCTTATATTAACACCACTGCTAGCAGCAACTGCTTGTGAGAAAT 720
 Qy 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyValAlaGlyProVal 200
 Db 721 GCCCGCGGGCACCGGGTCGCTATTTCACCTTACACCACTAGCCTGGGTGGTCCCTC 780
 Qy 201 SerIleSerAlaValAlaValLeuAlaPro 210
 Db 781 TCCATTCTCGCGTTGCGGTTTAGCCCCC 810

RESULT 9
 PCT-US95-13703-5
 ; Sequence 5, Application PC/TUS9513703
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND
 ; TITLE OF INVENTION: USES THEREFOR
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: P.O. Box 60850
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306-0850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/13703
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fabian, Gary R.
 ; REGISTRATION NUMBER: 33,875
 ; REFERENCE/DOCKET NUMBER: 4600-0293.41
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 324-0880
 ; TELEFAX: (415) 324-0960
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 984 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain) SG3
 ; INDIVIDUAL ISOLATE: region
 ; PCT-US95-13703-5

Mon Nov 1 10:49:17 2004

us-10-089-292a-2.rni

Alignment Scores: 8,38e-122 Length: 984
Pred. No.: 1076.00 Matches: 210
Score: 100.00% Conservativeness: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 98.26% Gaps: 0
DB: 5

US-10-089-292A-2 (1-213) x PCT-US95-13703-5 (1-984)

QY 1 GlnLeuPheTyrSerArgProValValSerAlaGlnGlyProThrValValLeuTyr 20
DB 181 CAGCTGTTCTACTCCGCTCCGCTTCTCTCAGCAATGGCGAGCGAGCTTTAAGTTGAT 240
QY 21 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 40
DB 241 ACATCTGTAGAGTAAGTCTCAGCAGGATAGGTTATGCAATCCCGCATGACATTCACCTC 300
QY 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
DB 301 CGAGAACTCTGTTGGTTATTTCAGGATTATGATAACCAACATGAACAAGATCGCGCAGC 360
QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTyrLeu 80
DB 361 CCTTCTCCAGCCCATCGCGCCCTTCTCTGCTTCGCTTCAGCTTAAGTGTCTTTGGCTC 420
QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
DB 421 TCTCTCAGCGTCCGAGTATGACCACTTATGGCTCTTCGACTGGCCCGACTTTAT 480
QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
DB 481 GTTCTGACTCTGTGACCTTGGTTAATGTGGACCGCGCGAGCGCGCTTCCCGTGC 540
QY 121 LeuAspThrThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
DB 541 CTGATTGGACCAAGTGCACATTGACGCTCGCCCTCTCCACCATCCAGCAGTACTCG 600
QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTyrGluAlaGlyThrThr 160
DB 601 AAGACCTTCTTGTCTCGCGCTCCGCGGTAAAGCTCTCTTCTGGAGGAGGACCAACT 660
QY 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 180
DB 661 AAAGCCGGGTACCTTATATTAATTAACACCACTGTAGCCCACTGCTTGTTCGAGAA 720
QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
DB 721 GCCGCGCGGCAACCGGTCGCTATTTCACCTTACACCACTAGCCTGGGTGCTGCTCCGTC 780

QY 201 SerLeuSerAlaValAlaValLeuAlaPro 210
DB 781 TCCATTTCTCGGTTGCGGTTTATAGCCCC 810

RESULT 10

US-08-259-148A-9
; Sequence 9, Application US/08259148A
; Patent No. 5741490
; GENERAL INFORMATION:
; APPLICANT: Reyes, Gregory R.
; APPLICANT: Bradley, Daniel W.
; APPLICANT: Twu, Jr-Shin
; APPLICANT: Turdy, Michael A.
; APPLICANT: Tam, Albert W.
; APPLICANT: Krawczynski, Krzysztof Z.
; APPLICANT: Yarbough, Patricia D.
; TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA

COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,148A
FILING DATE: 13-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUN-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0093.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1311 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: C2, BURNA, FIGURE 7
US-08-259-148A-9

Alignment Scores:
Pred. No.: 1,32e-121 Length: 1311
Score: 1076.00 Matches: 210
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 1 Gaps: 0

US-10-089-292A-2 (1-213) x US-08-259-148A-9 (1-1311)

QY 1 GlnLeuPheTyrSerArgProValValSerAlaGlnGlyProThrValValLeuTyr 20
DB 508 CAGCTGTTCTACTCCGCTCCGCTTGTCTCAGCAATGGCGAGCGAGCTTTAAGTTGAT 567
QY 21 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 40
DB 568 ACATCTGTAGAGTAAGTCTCAGCAGGATAGGTTATGCAATCCCGCATGACATTCACCTC 627
QY 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
DB 628 GGAGAACTCTGTTGGTTATTTCAGGATTATGATAACCAACATGAACAAGATCGCGCAGC 687
QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTyrLeu 80
DB 688 CCTTCTCCAGCCCATCGCGCCCTTCTCTGCTTCGAGCTTAATGATGTGCTTTGGCTC 747

QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
DB 748 TCTCTCAGCGTGCAGAGTATGACAGTCCACTTATGCTCTTCGACTGGCCAGTTTAT 807
QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
DB 808 GTTTCGTGACTCTGTGACCTTGTGTTAATGTTGCGACCGCGCGAGCGGTTGCCCGGTCG 867
QY 121 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
DB 868 CTCGATTGACCAAGTTCACACTTGACGGTGCCTCCCTCTCCACCATCCAGCAGTACTCG 927
QY 141 LysThrPheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 160
DB 928 AAGACCTTCTTTGTCTCGCGGTACGCTCTCTTTCTGGGAGGCGGCACAACT 987
QY 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuValGluAsn 180
DB 988 AAAGCGGGTACCCCTTATATTAATTAACACCACTGCTAGGACCAACTGCTTGTGAGAA 1047
QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
DB 1048 GCCGCGGCGACCGCGTGCCTATTTCCACTTACACCACTAGCTGGTGGTGGTCCCTC 1107
QY 201 SerIleSerAlaValAlaValLeuAlaPro 210
DB 1108 TCCATTTCGCGGTGCGGTTTGTAGCCGCC 1137
RESULT 11
US-08-484-054-9
; Sequence 9, Application US/08484054
; Patent No. 5770689
; GENERAL INFORMATION:
; APPLICANT: Reyes, Gregory R.
; APPLICANT: Bradley, Daniel W.
; APPLICANT: Twu, Jr-Shin
; APPLICANT: Purdy, Michael A.
; APPLICANT: Tam, Albert W.
; APPLICANT: Krawczynski, Krzysztof Z.
; TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,054
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 870,985
; FILING DATE: 20-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 822,335
; FILING DATE: 17-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 505,888
; FILING DATE: 05-APRIL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 420,921
; FILING DATE: 13-OCTOBER-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 367,486
; FILING DATE: 16-JUNE-1989

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 336,672
; FILING DATE: 11-APRIL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 208,997
; FILING DATE: 17-JUNE-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 4600-0093.38
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1311 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEetical: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: C2, BURMA, FIGURE 7
US-08-484-054-9

Alignment Scores:
Pred. No.: 1,32e-121 Length: 1311
Score: 1076.00 Matches: 210
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 1 Gaps: 0

US-10-089-292A-2 (1-213) x US-08-484-054-9 (1-1311)

QY 1 GlnLeuPheTyrSerArgProValValSerAlaGlnGlyGluProThrValLysLeuTyr 20
DB 508 CAGCTGTTCTACTCCGCTCCGTTGTCTCAGCCCAATGCGAGCCGACTGTTAAGTTGTAT 567
QY 21 ThrSerValGluAsnAlaGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 40
DB 568 ACATCTGTAGAGATGCTCAGCAGGATTAAGGTATGCAATCCCGCATGACATTGACCTC 627
QY 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
DB 628 GGAGAATCTCGTGTGTTATTTCAGGATTAATGATAACCAACATGAACAAGATCGGCGGACG 687
QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 80
DB 688 CTTTCTCCAGCCCATCGCGCCCTTTCTCTGCTCTTCGAGCTAATGATGCTTTGGCTC 747
QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
DB 748 TCTCTCAGCGTGCAGAGTATGACAGTCCACTTATGCTCTTCGACTGGCCAGTTTAT 807
QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
DB 808 GTTTCGTGACTCTGTGACCTTGTGTTAATGTTGCGACCGCGCGAGCGGCTTGGCGGTCG 867
QY 121 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
DB 868 CTCGATTGACCAAGGTCACACTTGACGGTGCCTCCCTCTCCACCATCCAGCAGTACTCG 927
QY 141 LysThrPheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 160
DB 928 AAGACCTTCTTTGTCTCGCGGTACGCTCTCTTTCTGGGAGGCGGCACAACT 987
QY 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuValGluAsn 180
DB 988 AAAGCGGGTACCCCTTATATTAATTAACACCACTGCTAGGACCAACTGCTTGTGAGAA 1047
QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200

Db 1048 GCCGCGGCGGCGGTCGCTATTTCCACTTACACCACTAGCTGGGTGCTGGTCCCGTC 1107
 Qy 201 SerlleSerAlaValAlaValAlaPro 210
 Db 1108 TCCATTTCTGCGGTGCGGTTTAGCCCCC 1137

RESULT 12

US-07-876-941A-9
 ; Sequence 9, Application US/07876941A
 ; Patent No. 5885768
 ; GENERAL INFORMATION:
 ; APPLICANT: Reyes, Gregory R.
 ; APPLICANT: Bradley, Daniel W.
 ; APPLICANT: Tam, Albert W.
 ; APPLICANT: Mitchell, Carl
 ; TITLE OF INVENTION: Hepatitis E Virus Peptide Antigen and
 ; TITLE OF INVENTION: Antibodies
 ; NUMBER OF SEQUENCES: 76
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: 350 Cambridge Avenue, Suite 250
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/876,941A
 ; FILING DATE: 01-MAY-1992
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 822,335
 ; FILING DATE: 17-JAN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 505,888
 ; FILING DATE: 05-APRIL-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 420,921
 ; FILING DATE: 13-OCTOBER-1989
 ; APPLICATION NUMBER: US 367,486
 ; FILING DATE: 16-JUNE-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 336,672
 ; FILING DATE: 11-APRIL-1989
 ; APPLICATION NUMBER: US 208,997
 ; FILING DATE: 17-JUNE-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sholtz, Charles K.
 ; REGISTRATION NUMBER: 38,615
 ; REFERENCE/DOCKET NUMBER: 4600-0093.33
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 324-0880
 ; TELEFAX: (415) 324-0960
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1311 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: C2, BURMA, FIGURE 7
 ; US-07-876-941A-9

Alignment Scores: 1.32e-121 Length: 1311
 Pred. No.:

Score: 1076.00 Matches: 210
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.26% Indels: 0
 DB: 2 Gaps: 0

US-10-089-292A-2 (1-213) x US-07-876-941A-9 (1-1311)

Qy 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 20
 Db 508 CAGCTGTTCTACTCCCGTCCGTTGCTCAGCAATGCGGAGCGGACTGTTAAGTTGAT 567
 Qy 21 ThrSerValGluAsnAlaGlnAspGlyGlyLeuAlaLeuProHisAspIleAspLeu 40
 Db 568 ACATCTGTAGAGATGCTCAGCAGGATAAGGTTATTGCAATCCCGCATGACATTGACCTC 627
 Qy 41 GlyClnSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
 Db 628 GGAGAATCTCGTGTGGTTATTTCAGGATTATGATACCAACATGAAACAGATCGGCCGACG 687
 Qy 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTyrIleu 80
 Db 688 CTTCTCCAGCCCATCGGCGCTTTCTCTGCTCTCGAGCTAATGATGCTTTGGCTC 747
 Qy 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
 Db 748 TCTCTCAGCGTGGCGAGTATGACACGTCCTTATGGCTCTTCGATGCGCCGATTTAT 807
 Qy 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
 Db 808 GTTTCAGCTCTGTGACCTTGTTAATGTTGCGACCGGCGGCGGCGGCTGTCGCGGTCG 867
 Qy 121 LeuAspTyrThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
 Db 868 CTCGATTGGACCAAGGTCACACTTGACGGTCGCGCCCTCTCCACCATCCAGCAGTACTCG 927
 Qy 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTyrGluAlaGlyThrThr 160
 Db 928 AAGACCTTTCTTTGCTGCGCTCGCGGTAAAGTCTCTTTCTGGGAGGAGGACCAACT 987
 Qy 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuValGluLys 180
 Db 988 AAAGCGGGGTACCTTATATATATACACCACTGCTAGCGACCACTGCTTTGTGCGAAT 1047
 Qy 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrSerLeuGlyAlaGlyProVal 200
 Db 1048 GCCGCGGCGGCGGCTCGCTATTTCCACTTACACCACTAGCTGGGTGCTGGTCCCGTC 1107

RESULT 13

US-07-870-985A-9
 ; Sequence 9, Application US/07870985A
 ; Patent No. 6455492
 ; GENERAL INFORMATION:
 ; APPLICANT: Reyes, Gregory R.
 ; APPLICANT: Bradley, Daniel W.
 ; APPLICANT: Twu, Jr-Shin
 ; APPLICANT: Purdy, Michael A.
 ; APPLICANT: Tam, Albert W.
 ; APPLICANT: Krawczynski, Krzysztof Z.
 ; TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: 350 Cambridge Avenue, Suite 250
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APRIL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1311 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: C2, BURMA, FIGURE 7
US-07-870-985A-9

Alignment Scores:
Pred. No.: 1,328-121 Length: 1311
Score: 1076.00 Matches: 210
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 4 Gaps: 0

US-10-089-292A-2 (1-213) x US-07-870-985A-9 (1-1311)

Qy 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 20
Db 508 CAGCTGTTCTACTCCGTCCTGCTCTCAGCAATGGCGAGCCGACTGTAAGTTGTAT 567

Qy 21 ThrSerValGluAsnAlaGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 40
Db 568 ACATCTGTAGAGATGCTCAGCAGGATAAGGTATTCGAATCCCGCATGACATTGACCTC 627

Qy 41 GlyGluSerArgValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
Db 628 GGAGAATCTCGTGTGTTATTTCAGATTATGATAACCAACATGAACAGATCGGCCGACG 687

Qy 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTyrLeu 80
Db 688 CTTCTCCAGCCCATCGGCCCTTCTCTGCTTCCTTCAGCTAATGATGCTTTGGCTC 747

Qy 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
Db 811 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100

Db 748 TCTCTCACCCTGCCGAGTATGACCACTTATGGCTTTCGACTGGCCCGCTTAT 807

Qy 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
Db 808 GTTTCCTGACTCTGTGACCTTGGTTAATGTTGCGACCGCGCAGGCGGTTGCCCGGTG 867

Qy 121 LeuAspTyrThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnTyrSer 140
Db 868 CTCGATTGGACCAAGGTACACTTGGCGGTGCGCCCTCTCCACCATCCACGACTACTCG 927

Qy 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTyrGluAlaGlyThrThr 160
Db 928 AAGACCTTCTTTGTCTCCCTCCGCGGTAAAGCTCTCTTCTGGGAGGAGGACCAACT 987

Qy 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuValGluAsn 180
Db 988 AAGCCCGGTACCTTATATTAACACCACTGCTAGCGACCAACTGCTTGTGCGAAT 1047

Qy 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
Db 1048 GCCCGCGGACCGGTCGCTATTTCACCTTACACCACTAGCTGGGTGCTGGTCCCGTC 1107

Qy 201 SerIleSerAlaValAlaValLeuAlaPro 210
Db 1108 TCCATTCTCGCGGTGCGGTTTAGCCCCC 1137

RESULT 14
US-08-542-634-3
Sequence 3, Application US/08542634
Patent No. 6214970
GENERAL INFORMATION:
APPLICANT: Fuerst, Thomas R.
APPLICANT: McAtee, C. Patrick
APPLICANT: Yarbough, Patrice O.
APPLICANT: Zhang, Yifan
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542,634
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1647 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Hepatitis E virus (Burma) r62kDa,
INDIVIDUAL ISOLATE: FIGURE 2
US-08-542-634-3

Alignment Scores:

Pred. No.:	1.9e-121	Length:	1647
Score:	1076.00	Matches:	210
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	98.26%	Indels:	0
DB:	3	Gaps:	0

US-10-089-292A-2 (1-213) X US-08-542-634-3 (1-1647)

Qy	1	GlnLeuPheTyrSerArgProValSerAlaAsnGlyGluProThrValLysLeuTyr	20
Db	847	CAGCTGTCTACTCCGCTCCGTTGTCTCAGCAATGGCGAGCGCACTGTTAAAGTTGTAT	906
Qy	21	ThrSerValGluAsnAlaGlnGlnAspLysGlyLeaIleProHisAspIleAspLeu	40
Db	907	ACATCTGTAGAGAAATGCTCAGCAGGATAGGGTATTGCAATCCCGATGACATGACCTC	966
Qy	41	GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr	60
Db	967	GGAGAATCTCGTCTGGTTATTACAGGATTATGATAAACCAACATGAACAAGATCGCCGACG	1026
Qy	61	ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu	80
Db	1027	CCTTCTCCAGCCCAATCGGCCCTTTCTCTGTCTCTCGAGCTAATGATGTCTTTGGCTC	1086
Qy	81	SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr	100
Db	1087	TCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCACTTAT	1146
Qy	101	ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer	120
Db	1147	GTTTCTGACTCTGTGACCTTGGTTAATGTTGCACCGCGCGAGGCGGTGGCCGCTCG	1206
Qy	121	LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnTyrSer	140
Db	1207	CTCGATTGACCAAGGTACACTTGACGTTGCCGCCCTCTCCACCATCCAGCAGTACTCG	1266
Qy	141	LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr	160
Db	1267	AAGACCTTCTTTGCTCTGCCGCTCCGCGGTAAAGCTCTCTTTCTGGGAGGCGAGCACACT	1326
Qy	161	LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn	180
Db	1327	AAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTGTGCGAGAAT	1386
Qy	181	AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal	200
Db	1387	GCGCCCGGACACCGGTCGTATTTCCACTTACACCACTAGCCCTGGGTGTCGTCCGTC	1446
Qy	201	SerIleSerAlaValAlaValLeuAlaPro	210
Db	1447	TCCATTTCTCGGTTGCGGTTTTAGCCCCC	1476

RESULT 15

RESOL 13
UIS-08-477-292-3

09-08-47-292-3 : Sequence 3 Application IIS/08477292

Sequence 3, Application No. 6291641

; FACILE NO. 6291641
; GENERAL INFORMATION:

GENERAL INFORMATION:
APPLICANT: Everett Thomas

APPLICANT: Fuerst, Thomas

APPLICANT: McAttee, Patrick

APPLICANT: Yarbough, Pa

APPLICANT: Zhang, Yifan

10 TITLE OF INVENTION: Hep

; NUMBER OF SEQUENCES: 24
; GOVERNOR: BROWN, RICHARD L.
; COUNTY: ALBANY
; DISTRICT: 06
; OFFICE: SENATE
; TERM: 2007-2009
; PARTY: REPUBLICAN
; GENDER: M
; AGE: 58
; ETHNICITY: W
; RELIGION: C
; EDUCATION: GRADUATE
; OCCUPATION: ATTORNEY
; EMPLOYER: STATE OF NEW YORK
; ADDRESS: 100 NASSAU ST., 10TH FLOOR
; CITY: NEW YORK
; STATE: NY
; ZIP: 10038
; PHONE: 212-462-2400
; FAX: 212-462-2400
; EMAIL: RICHARD.BROWN@SENATE.NY.GOV
; WEBSITE: WWW.RICHARDBROWN.NY.GOV
; BIOGRAPHICAL SKETCH:
RICHARD L. BROWN was born on May 1, 1950, in Albany, New York. He graduated from Albany High School in 1968 and received his Bachelor's degree in Political Science from Albany State University in 1972. He earned his Juris Doctor from Albany Law School of Saint Joseph's University in 1975. Mr. Brown has been practicing law since 1975, primarily in the areas of criminal defense and civil litigation. He is currently a partner in the law firm of Brown & Associates, P.C., where he specializes in representing individuals and businesses in criminal matters. Mr. Brown is also a frequent speaker at legal seminars and conferences. He is active in the community and serves as a member of the Albany County Bar Association and the New York State Bar Association. In addition, he is a past president of the Albany County Chamber of Commerce. Mr. Brown is married and has two children.

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Cathleen M. Desjardins

STREET: 505 Penobscot

; CITY: Redwood

; STATE: CA

; COUNTRY: US

; ZIP: 94063

Qy 161 LysAlaGlyTyrProTyrAsnThrThrAlaSerAspGlnLeuValGluAsn 180
Db |||||||
Qy 1327 AAAGCCGGGTACCCCTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTGAGAAT 1386
Db |||||||
Qy 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
Db |||||||
Qy 1387 GCCGCCGGGCACCGGGTCGCTATTTCACCTTACACCACTAGCCTGGGTGCTGCCGTC 1446
Db |||||||
Qy 201 SerIleSerAlaValAlaValLeuAlaPro 210
Db |||||||
Qy 1447 TCCATTTCTGCGGTTGCCGTTTTAGCCCCC 1476
Db |||||||

Search completed: October 28, 2004, 11:55:03
Job time : 73 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 28, 2004, 09:51:24 ; Search time 2714 Seconds

(without alignments)
3711.388 Million cell updates/sec

Title: US-10-089-292A-2

Perfect score: 1095
Sequence: 1 QLFYRPPVWSANGPTVKLY.....SLGAGPVSISSAVLAPPPR 213

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2_1/USPTO_epool/US10089292/runat_27102004_153927_10154/app_query.fasta_1.391
-DB=GenEmbl -QWMT=fastap -SUPFIX=rge -MINMATCH=0.1 -LOECL=0 -LOEEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1076	98.3	803	6	AR278919 Sequence
2	1076	98.3	984	6	AR002164 Sequence
3	1076	98.3	984	6	AR170408 Sequence
4	1076	98.3	984	6	I73145 Sequence 7

5	1076	98.3	984	6	AR232469	AR232469 Sequence
6	1076	98.3	1117	14	HEU40044	U00044 Hepatitis E
7	1076	98.3	1311	6	AR002166	AR002166 Sequence
8	1076	98.3	1311	6	AR232471	AR232471 Sequence
9	1076	98.3	1647	6	AR170406	AR170406 Sequence
10	1076	98.3	1647	6	E17105	E17105 DNA encodin
11	1076	98.3	1658	6	AR278918	AR278918 Sequence
12	1076	98.3	1686	6	AR278920	AR278920 Sequence
13	1076	98.3	1946	14	HEVBCN6	AF058684 Hepatitis E
14	1076	98.3	1983	6	E17107	E17107 Hepatitis E
15	1076	98.3	1983	6	I73139	I73139 Sequence 1
16	1076	98.3	1984	6	AR278906	AR278906 Sequence
17	1076	98.3	2049	6	AR002160	AR002160 Sequence
18	1076	98.3	2049	6	AR170404	AR170404 Sequence
19	1076	98.3	2049	6	AR232465	AR232465 Sequence
20	1076	98.3	2094	6	AR002158	AR002158 Sequence
21	1076	98.3	2094	6	AR232463	AR232463 Sequence
22	1076	98.3	2173	14	AF065061	AF065061 Hepatitis E
23	1076	98.3	2173	14	HPEA	M05081 Hepatitis E
24	1076	98.3	2143	14	AF185822	AF185822 Hepatitis E
25	1076	98.3	2168	6	AR139826	AR139826 Sequence
26	1076	98.3	2168	6	AR167470	AR167470 Sequence
27	1076	98.3	2168	6	AR234194	AR234194 Sequence
28	1076	98.3	2168	6	AR476111	AR476111 Sequence
29	1076	98.3	2168	6	AR487996	AR487996 Sequence
30	1076	98.3	2168	6	BD084498	BD084498 Recombina
31	1076	98.3	2194	6	E17109	E17109 Hepatitis E
32	1076	98.3	2195	6	AR150915	AR150915 Sequence
33	1076	98.3	2195	6	AR207633	AR207633 Sequence
34	1076	98.3	2204	14	AF444002	AF444002 Hepatitis E
35	1076	98.3	2204	14	AF444003	AF444003 Hepatitis E
36	1076	98.3	2207	14	HPECG	D11092 Hepatitis E
37	1076	98.3	2207	14	HPEVSP	M73218 Hepatitis E
38	1076	98.3	2212	14	AY230202	AY230202 Hepatitis E
39	1072	97.9	1983	14	AF124407	AF124407 Hepatitis E
40	1072	97.9	2104	14	AF051351	AF051351 Hepatitis E
41	1072	97.9	2193	14	HPEGENA	L25547 Hepatitis E
42	1072	97.9	2202	14	HEVCG	X98292 Hepatitis E
43	1072	97.9	7206	14	AF459438	AF459438 Hepatitis E
44	1072	97.9	7221	14	HPEORFS	L25595 Hepatitis E
45	1071	97.8	2106	14	AF051352	AF051352 Hepatitis E

ALIGNMENTS

RESULT 1	AR278919	Sequence 17 from patent US 6514690.	803 bp	DNA	linear	PAT 10-APR-2003
LOCUS	AR278919					
DEFINITION	Sequence 17 from patent US 6514690.					
ACCESSION	AR278919					
VERSION	AR278919.1	GI:29713553				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 803)					
AUTHORS	Li, F., Hui, Z., Anderson, D.A., Logarini, S.A. and Torresi, J.					
TITLE	Immunoreactive antigens of Hepatitis E Virus					
JOURNAL	Patent: US 6514690-A 17 04-FEB-2003;					
FEATURES	source					
	1..803					
	/organism="unknown"					
	/mol_type="genomic DNA"					
ORIGIN						

Alignment Scores:						
Pred. No.:	1.79e-91	Length:	803			
Score:	1076.00	Matches:	210			
Percent Similarity:	100.00%	Conservative:	0			
Best Local Similarity:	100.00%	Mismatches:	0			
Query Match:	98.26%	Indels:	0			
DB:	6	Gaps:	0			

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QY 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValIysLeuTyr 20
DB 1 CAGCTGTTCTACTCTCGTCCGCTGCTCTCAGCAATGGCGAGCCGACTGTTAAGCTTTAT 60
QY 21 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 40
DB 61 ACATCTGTAGAGATGCTCAGCAGATAGAGGTATTGCAATCCCGCATGACATGACCTC 120
QY 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
DB 121 GGGAGTCTCGTGTAGTTATTTCAGGATTATGACAAACCAACATGACGAGCCGACGACA 180
QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 80
DB 181 CCTTCCCGAGCCCATCGCGCCCTTTCTGTCCTCCGAGCTAAATGATGTGCTTTGGCTT 240
QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
DB 241 TCTCTACCGCTGCGAGTATGACAGTCCACTTACGGCTCTTCGACCGGCCGACTCTAT 300
QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
DB 301 GTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGCGCGCAGCGCGCTTGCCCGGTCA 360
QY 121 LeuAspThrThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
DB 361 CTCGACTGACCAAGGTCACTTGTATGCTGCGCCCTTTCCACCATCCAGCAGTATTCAC 420
QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheThrGluAlaGlyThrThr 160
DB 421 AGACCTCTTTGCTGCTCGCTCGCGGTAGCTCTCTTTGGGAGCAGGTACTACT 480
QY 161 LysAlaGlyTyrProTyrAsnTyrAsnThrAlaSerAspGlnLeuValGluAsn 180
DB 481 AAAGCGGGTACCTTATATTAATTAACACCACTGCTAGTGACCAACTGCTCGTTCGAGAT 540
QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
DB 541 GCGCTGGGCGATCGGCTTCTATTTCCACTTACACCACTAGCTGGGTCTGGTCCCGTC 600
QY 201 SerIleSerAlaValAlaValLeuAlaPro 210
DB 601 TCTATTTCCGCGTGTCTGTTTAGCCCCC 630

RESULT 2
AR002164
LOCUS AR002164
DEFINITION Sequence 7 from patent US 5741490.
ACCESSION AR002164
VERSION AR002164.1 GI:3963718
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 984)
AUTHORS Reyes,G.R.; Bradley,D.W.; Twu,J.-S.; Purdy,M.A.; Tam,A.W.;
TITLE Krawczynski,K.Z. and Yarbough,P.D.
JOURNAL Hepatitis E virus vaccine and method
PATENT: US 5741490-A 7 21-APR-1998;
FEATURES
LOCATION/Qualifiers
1..984
source
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 2,34e-91 Length: 984
Score: 1076.00 Matches: 210
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
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DB: 6 Gaps: 0
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QY 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValIysLeuTyr 20
DB 181 CAGCTGTTCTACTCTCGCTCCGTTGTCTCAGCAATGGCGAGCCGACTGTTAAGTTGAT 240
QY 21 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 40
DB 241 ACATCTGTAGAGATGCTCAGCAGATAGAGGTATTGCAATCCCGCATGACATGACCTC 300
QY 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
DB 301 GGAGAACTCTCGTGTGTTATTTCAGGATTATGATAACCAACATGAACAGATCGGCCGACG 360
QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 80
DB 361 CCTTCTCCAGCCCATCGCGCCCTTTCTCTGCTCCTCGAGCTAAATGATGTGCTTTGGCTC 420
QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
DB 421 TCTCTACCGCTGCGAGTATGACAGTCCACTTATGAGCTCTTCGACTGGCCGACTTTAT 480
QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
DB 481 GTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGCGCGCAGCGCGCTTGCCCGGTCC 540
QY 121 LeuAspThrThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
DB 541 CTCGATTCCGACCAAGGTCACTTGTACCGGTGCGCCCTCTCCACCATCCAGCAGTACTCG 600
QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheThrGluAlaGlyThrThr 160
DB 601 AAGACCTCTTTGCTGCTCGCTCGCGGTAGCTCTCTTTGGGAGCAGCAGCAACT 660
QY 161 LysAlaGlyTyrProTyrAsnTyrAsnThrAlaSerAspGlnLeuValGluAsn 180
DB 661 AAAGCGGGTACCTTATATTAATTAACACCACTGCTAGTGACCAACTGCTGTCGAGAT 720
QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
DB 721 GCGCGCGGCGATCGGCTTCTATTTCCACTTACACCACTAGCTGGGTCTGGTCCCGTC 780
QY 201 SerIleSerAlaValAlaValLeuAlaPro 210
DB 781 TCCATTTCTCGGTTGCGGTTTAGCCCCC 810

RESULT 3
AR170408
LOCUS AR170408
DEFINITION Sequence 5 from patent US 6291641.
ACCESSION AR170408
VERSION AR170408.1 GI:17908367
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 984)
AUTHORS Fuerst,T.R., McAtee,C.Patrick., Yarbough,P.O. and Zhang,Y.-F.
TITLE Hepatitis E virus antigens and uses therefor
JOURNAL Patent: US 6291641-A 5 18-SEP-2001;
FEATURES
LOCATION/Qualifiers
1..984
source
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 2,34e-91 Length: 984
Score: 1076.00 Matches: 210
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Query Match: 98.26% Indels: 0
DB: 6 Gaps: 0

US-10-089-292A-2 (1-213) x AR170408 (1-984)

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Db 181 CAGCTGTTCTACTCCCGTCCGTTGTCTCAGCCAATGGCGAGCGACTGTTAAGTTGTAT 240
Qy 21 ThrSerValGluAsnAlaGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 40
Db 241 ACATCTGTAGAGATGCTCAGCAGATAAGGTAATGCAATCCCGCATGACATTGACCTC 300
Qy 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
Db 301 GGAGAATCTCGTGTGGTTATTTCAGATTATGATAACCAACATGAACAGATCGGCCGACG 360
Qy 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTyrLeu 80
Db 361 CCTTCTCCAGCCCATCGGCCCTTCTCTGTCTTCGAGCTAATGATGCTTTGGCTC 420
Qy 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
Db 421 TCTCTCACCGTCCGAGTATGACAGTCCACTTATGCTCTTCGACTGGCCAGTTTAT 480
Qy 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
Db 481 GTTCTTGACTCTGTGACCTTGTGTAATGTTGCGACCGCGCGCAGCGCGTTCGCCGCTG 540
Qy 121 LeuAspTyrThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
Db 541 CTCGATTGGAACAAGGTCACTTGACGGTCCGCCCTCTCCACCATCAGCAGTACTCG 600
Qy 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTyrGluAlaGlyThrThr 160
Db 601 AAGACCTCTTGTGCTCCGCTCCGCGTAAAGTCTCTTCTGGAGGCGAGGCACAACT 660
Qy 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 180
Db 661 AAAGCCGGGTACCTTATAATTATAACACCACTGCTAGCAGCAACTGCTTGTGAGAAAT 720
Qy 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
Db 721 GCCCGCGGCAACCGGTCGCTATTTCACCTTACACCACTAGCTGGGTGCTGGTCCCGTC 780
Qy 201 SerIleSerAlaValAlaValLeuAlaPro 210
Db 781 TCCATTCTCGGGTGGCGTTTATAGCCCCC 810
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RESULT 4

LOCUS I73145 984 bp DNA linear PAT 03-APR-1998

DEFINITION Sequence 7 from patent US568239

ACCESSION I73145

VERSION I73145.1 GI:3009284

KEYWORDS

SOURCE Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 984)

AUTHORS Reyes,G.R., Tam,A.W. and Yarbough,P.O.

TITLE Hepatitis E virus peptides and methods

JOURNAL Patent: US 568239-A 7 11-NOV-1997;

FEATURES Location/Qualifiers

source 1. 984

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores: 2.34e-91 Length: 984

Pred. No.: 1076.00 Matches: 210

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 6 Gaps: 0

US-10-089-292A-2 (1-213) x I73145 (1-984)

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Qy 21 ThrSerValGluAsnAlaGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 40
Db 241 ACATCTGTAGAGATGCTCAGCAGATAAGGTAATGCAATCCCGCATGACATTGACCTC 300
Qy 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
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Qy 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
Db 421 TCTCTCACCGTCCGAGTATGACAGTCCACTTATGCTCTTCGACTGGCCAGTTTAT 480
Qy 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
Db 481 GTTCTTGACTCTGTGACCTTGTGTAATGTTGCGACCGCGCGCAGCGCGTTCGCCGCTG 540
Qy 121 LeuAspTyrThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
Db 541 CTCGATTGGAACAAGGTCACTTGACGGTCCGCCCTCTCCACCATCAGCAGTACTCG 600
Qy 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTyrGluAlaGlyThrThr 160
Db 601 AAGACCTCTTGTGCTCCGCTCCGCGTAAAGTCTCTTCTGGAGGCGAGGCACAACT 660
Qy 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 180
Db 661 AAAGCCGGGTACCTTATAATTATAACACCACTGCTAGCAGCAACTGCTTGTGAGAAAT 720
Qy 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
Db 721 GCCCGCGGCAACCGGTCGCTATTTCACCTTACACCACTAGCTGGGTGCTGGTCCCGTC 780
Qy 201 SerIleSerAlaValAlaValLeuAlaPro 210
Db 781 TCCATTCTCGGGTGGCGTTTATAGCCCCC 810
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RESULT 5

LOCUS AR232469

DEFINITION Sequence 7 from patent-US-6455492

ACCESSION AR232469

VERSION AR232469.1 GI:27274538

KEYWORDS

SOURCE Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 984)

AUTHORS Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,

Krawczynski,K.Z. and Yarbough,P.O.

TITLE Hepatitis E virus vaccine and method

JOURNAL Patent: US 6455492-A 7 24-SEP-2002;

FEATURES Location/Qualifiers

source 1. 984

/organism="unknown"

/mol_type="mRNA"

ORIGIN

Alignment Scores: 2.34e-91 Length: 984

Pred. No.: 2.34e-91 Length: 984

Score:	1076.00	Matches:	210
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	98.26%	Indels:	0
DB:	6	Gaps:	0
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QY	1	GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValIysLeuTyr	20
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QY	21	ThrSerValGluAsnAlaGlnGlnAspIysGlyIleAlaIleProHisAspIleAspLeu	40
Db	241	ACATCTGTAGAGATGCTCAGCAGATAGAGTATTGCAATCCCGCATGACATTGACCTC	300
QY	41	GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr	60
Db	301	GGAGAATCTCGTGTGTTATTGAGTATTGATGATACCAACATGAACAGATCGGCCGACG	360
QY	61	ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu	80
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QY	81	SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr	100
Db	421	TCTCTCACCGCTGCCGAGTATGACCACTTATGCTTTCGACTGGCCAGTTTAT	480
QY	101	ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer	120
Db	481	GTITCTGACTCTGTGACCTTGGTTAATGTTGGACCGCGCGAGCGCGTTCGCCGGTGC	540
QY	121	LeuAspTrpThrIysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer	140
Db	541	CTCGATTGACCAAGGTACACTTGACGTCGCCGCCCTCTCCACCATCCAGGACTCG	600
QY	141	LysThrPhePheValLeuProLeuArgGlyIysLeuSerPheTrpGluAlaGlyThrThr	160
Db	601	AAGACCTTCTTGTCTCGCGCTCCGCGTAAAGTCTCTTTCTGGGAGGCAGGCACAACT	660
QY	161	LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuValGluAsn	180
Db	661	AAAGCCGGGTACCTTTATATATATACACCACTGTAGCGACCACTGCTTGTGAGAAAT	720
QY	181	AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal	200
Db	721	GCGCCGGGACCGGTCGCTATTTCCATTACACCACTAGCTGGGTCTGGTCCCGTTC	780
QY	201	SerIleSerAlaValAlaValLeuAlaPro	210
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RESULT 6			
HEU40044			
LOCUS			
DEFINITION			
Hepatitis E virus structural protein 2 (orf2) mRNA, partial cds.			
U40044			
ACCESSION			
VERSION			
U40044.1 GI:4096791			
KEYWORDS			
Hepatitis E virus			
SOURCE			
Hepatitis E virus			
ORGANISM			
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepatitis E-like viruses.			
REFERENCE			
1 (bases 1 to 1117)			
AUTHORS			
Van Cuyck-Gandre, H., Clements, N.J., Zhang, H.Y., Caudill, J.C., Cohen, S.G., Coursaget, P., Buisson, Y., Warren, R.L. and Longer, C.F.			
TITLE			
Partial Sequence of HEV Isolates from North Africa and Pakistan: Comparison with Known HEV Sequences			
JOURNAL			
Unpublished			
REFERENCE			
2 (bases 1 to 1117)			
AUTHORS			
Van Cuyck-Gandre, H., Clements, N.J., Zhang, H.Y., Caudill, J.C., Cohen, S.G., Coursaget, P., Buisson, Y., Warren, R.L. and Longer, C.F.			
TITLE			
Direct Submission			
JOURNAL			
Unpublished			
REFERENCE			
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AUTHORS			
Van Cuyck-Gandre, H., Clements, N.J., Zhang, H.Y., Caudill, J.C., Cohen, S.G., Coursaget, P., Buisson, Y., Warren, R.L. and Longer, C.F.			
TITLE			
Direct Submission			
JOURNAL			
Unpublished			
REFERENCE			
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AUTHORS			
Van Cuyck-Gandre, H., Clements, N.J., Zhang, H.Y., Caudill, J.C., Cohen, S.G., Coursaget, P., Buisson, Y., Warren, R.L. and Longer, C.F.			
TITLE			
Direct Submission			
JOURNAL			
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AUTHORS			
Van Cuyck-Gandre, H., Clements, N.J., Zhang, H.Y., Caudill, J.C., Cohen, S.G., Coursaget, P., Buisson, Y., Warren, R.L. and Longer, C.F.			
TITLE			
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Van Cuyck-Gandre, H., Clements, N.J., Zhang, H.Y., Caudill, J.C., Cohen, S.G., Coursaget, P., Buisson, Y., Warren, R.L. and Longer, C.F.			
TITLE			
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Van Cuyck-Gandre, H., Clements, N.J., Zhang, H.Y., Caudill, J.C., Cohen, S.G., Coursaget, P., Buisson, Y., Warren, R.L. and Longer, C.F.			
TITLE			
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AUTHORS			
Van Cuyck-Gandre, H., Clements, N.J., Zhang, H.Y., Caudill, J.C., Cohen, S.G., Coursaget, P., Buisson, Y., Warren, R.L. and Longer, C.F.			
TITLE			
Direct Submission			
JOURNAL			
Unpublished			
REFERENCE			
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AUTHORS			
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TITLE			
Direct Submission			
JOURNAL			
Unpublished			
REFERENCE			
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AUTHORS			
Van Cuyck-Gandre, H., Clements, N.J., Zhang, H.Y., Caudill, J.C., Cohen, S.G., Coursaget, P., Buisson, Y., Warren, R.L. and Longer, C.F.			
TITLE			
Direct Submission			
JOURNAL			
Unpublished			
REFERENCE			
200			
AUTHORS			
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TITLE			
Direct Submission			
JOURNAL			

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DEFINITION Sequence 9 from patent US 5741490-A
ACCESSION AR002166
VERSION AR002166.1 GI:3963720
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
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Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
Krawczynski,K.Z. and Yarbough,P.D.
TITLE Hepatitis E virus vaccine and method
JOURNAL Patent: US 5741490-A 9 21-APR-1998;
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ACCESSION AR232471
VERSION AR232471.1 GI:27274540
KEYWORDS
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ORGANISM Unknown.
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Krawczynski,K.Z. and Yarbough,P.O.
TITLE Hepatitis E virus vaccine and method
JOURNAL Patent: US 6455492-A 9 24-SEP-2002;
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Best Local Similarity: 100.00% Mismatches: 0
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DB 1108 TCCATTCTCGCGTTGCCGTTTTCAGCCCC 1137

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DEFINITION Sequence 3 from patent US 6291641.
ACCESSION ARI170406
VERSION ARI170406.1 GI:17908365
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1647)
AUTHORS Fuerst,T.R., McAtee,C.Patrick., Yarbough,P.O. and Zhang,Y.-F.
TITLE Hepatitis E virus antigens and uses therefor
JOURNAL Patent: US 6291641-A 3 18-SEP-2001;
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
Gaps: 6

US-10-089-292A-2 (1-213) x ARI170406 (1-1647)

QY 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 20
DB 847 CAGCTGTTCTACTCCGTCCTCGCTGCTCAGCAATGGCGAGCCGACTGTTAAGTTGTAT 906

QY 21 ThrSerValGluAsnAlaGlnGlnAspTyrGlyIleAlaIleProHisAspIleAspLeu 40
DB 907 ACATCTGTAGAGATGCTCAGCAGGATAGGGTATTGCAATCCCGCATGACATTGACCTC 966

QY 41 GlyGluSerArgValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
DB 967 GGAGAAATCTCGTGGTTATTGAGGATTATGATAACCAACATGAACAGATCGGCGGAGC 1026

QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTyrLeu 80
DB 1027 CTTCTCCAGCCCATCGCGCTTCTCTGCTTCTCGAGCTAATGATGTGCTTTGGCTC 1086

QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
DB 1087 TCTCTCACCGCTGCCGAGTATGACAGTCCACTTATGGCTCTTCGACTGGCCGAGTTTAT 1146

QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
DB 1147 GTTCTCGACTCTGTGACCTTGGTTAATGTTGGACCGGCGGAGCCGCTTCCCGGTCG 1206

QY 121 LeuAspTyrThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
DB 1207 CTCGATTGACCAAGTCCACTTACGCGTGGCCCTCTCCACCATCCAGCAGTACTCG 1266

QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTyrGluAlaGlyThrThr 160
DB 1267 AAGACCTCTCTTGTCTCGCGCTCCGCGGTAAAGCTCTCTTCTGGGAGGAGCGACCACT 1326

QY 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuValGluAsn 180

DB 1327 AAAGCCGGTACCCCTTATATATATATACACCACTGCTAGCACCACCACTGCTTGTGAGAAAT 1386

QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
DB 1387 GCCGCGGACCGGGTGGCTATTTCCACTTACACCACTAGCGTGGTGGTCCCGTC 1446

QY 201 SerIleSerAlaValAlaValLeuAlaPro 210
DB 1447 TCCATTCTCGCGTTGCCGTTTTCAGCCCC 1476

RESULT 10
E17105
LOCUS E17105 1647 bp DNA linear PAT 28-JUL-1999
DEFINITION DNA encoding HEV hollow particle.
ACCESSION E17105
VERSION E17105.1 GI:5711788
KEYWORDS JP 1998234383-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1647)
AUTHORS Takeda,N., Ri,T. and Miyamura,T.
TITLE HEPATITIS E VIRUS HOLLOW PARTICLE, GENE ENCODING THE SAME AND PREPARATION OF RECOMBINATION VECTOR CONTAINING THE GENE AND UTILIZATION OF THE RECOMBINATION VECTOR
JOURNAL Patent: JP 1998234383-A 1 08-SEP-1998;
COMMENT DENKA SEIKEN CO LTD, KOKURITSU KANSENSHIYOU KENKYUSHO
OS Hepatitis E virus
PN JP 1998234383-A/1
PD 08-SEP-1998
PF 28-FEB-1997 JP 1997062445
PI TAKEDA NAOKAZU, RI TENSEI, MIYAMURA TATSUO
PC C12N15/09,C07K14/08,C12N5/10,C12P21/02;
CC strandedness: Double;
CC topology: Linear;
FH Key : Location/Qualifiers
FH
FT source 1. .1647
FT /organism='Hepatitis E virus' FT mat_peptide
FT 1. .1647 /product='hollow particle'.
FEATURES
source
1. .1647
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Alignment Scores:
Pred. No.: 4.59e-91 Length: 1647
Score: 1076.00 Matches: 210
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
Gaps: 6

US-10-089-292A-2 (1-213) x E17105 (1-1647)

QY 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 20
DB 847 CAGCTGTTCTACTCCGTCCTCGCTGCTCAGCAATGGCGAGCCGACTGTTAAGTTGTAT 906

QY 21 ThrSerValGluAsnAlaGlnGlnAspTyrGlyIleAlaIleProHisAspIleAspLeu 40
DB 907 ACATCTGTAGAGATGCTCAGCAGGATAGGGTATTGCAATCCCGCATGACATTGACCTC 966

QY 41 GlyGluSerArgValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
DB 967 GGAGAAATCTCGTGGTTATTGAGGATTATGATAACCAACATGAACAGATCGGCGGAGC 1026

QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTyrLeu 80
DB 1027 CTTCTCCAGCCCATCGCGCTTCTCTGCTTCTCGAGCTAATGATGTGCTTTGGCTC 1086

QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
Db 1087 TCTCTCACCGCTGCCAGTATGACAGTCCACTTATGGCTCTTCGACTGGCCAGTTAT 1146
QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
Db 1147 GTTCTGTGACTCTGTGACCTTGGTTAATGTTGGACCGCGCGAGCGCTTGCCCGGTG 1206
QY 121 LeuAspTprThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
Db 1207 CTCGATTGACCAAGTCCACTTGACGTCGCCCCCTCTCCACCATCCAGCAGTACTCG 1266
QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTprGluAlaGlyThrThr 160
Db 1267 AAGACCTTCTTGTCTCGCTCGCGGTAAAGTCTCTTTCTGGGAGCGACCAACT 1326
QY 161 LysAlaGlyTyrProTyrAsnThrThrAlaSerAspGlnLeuValGluAsn 180
Db 1327 AAAGCCGGGTACCCCTTAATTAATTAACACCACTGCTAGCACCACACTGCTGTGAGAA 1386
QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrSerLeuGlyAlaGlyProVal 200
Db 1387 GCCGCGCGGACCGGCTGCTATTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTC 1446
QY 201 SerIleSerAlaValAlaValLeuAlaPro 210
Db 1447 TCCATCTCGCGGTGCTGCTTTAGCCCCC 1476

RESULT 11
AR278918 1658-bp DNA linear PAT 10-APR-2003
LOCUS AR278918 Sequence 15 from patent-US-6514690.
DEFINITION AR278918
ACCESSION AR278918
VERSION AR278918.1 GI:29713552
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1658)
AUTHORS Li, F., Hui, Z., Anderson, D.A., Logarini, S.A. and Torresi, J.
TITLE Immunoreactive antigens of Hepatitis E Virus
JOURNAL Patent: US 6514690-A 15 04-FEB-2003;
FEATURES Location/Qualifiers
source 1..1658
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 4,636-91 Length: 1658
Score: 1076.00 Matches: 210
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 6 Gaps: 0
US-10-089-292A-2 (1-213) x AR278918 (1-1658)

QY 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 20
Db 884 CAGCTGTTCTACTCTCGTCCCGCTCTCAGCAATGGCGAGCCGACTGTTAAGCTTTAT 943
QY 21 ThrSerValGluAsnAlaGlnAspLysGlyIleAlaIleProHisAspLeu 40
Db 944 ACATCTGAGAAATGCTCAGCAGATAAGGTAATGCAATCCCGATGACATCGACCTC 1003
QY 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
Db 1004 GGGAGTCTCGTGTAGTATTTCAGATTATGACACCAACATGACAGACCGACCGACA 1063
QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 80

Db 1064 CTTCCCCAGCCCATCGCGCCCTTTTCTGTCTCCGAGTAATGATGTGCTTGGCTT 1123
QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
Db 1124 TCTCTCACCGCTGCCAGTATGACAGTCCACTTACGGCTCTTCGACCGGCCAGTCTAT 1183
QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
Db 1184 GTCTCTGACTCTGTGACCTTGGTTAATGTTGGACCGCGCGAGCGCTTGCCCGGTCA 1243
QY 121 LeuAspTprThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
Db 1244 CTCGACTGACCAAGTCCACTTGATGCTGCCCTTTCCACCATCCAGCAGTATTCA 1303
QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTprGluAlaGlyThrThr 160
Db 1304 AAGACCTTCTTGTCTCGCTCGCGGTAAAGTCTCTCTTTGGGAGCGAGTACTACT 1363
QY 161 LysAlaGlyTyrProTyrAsnThrThrAlaSerAspGlnLeuValGluAsn 180
Db 1364 AAAGCCGGGTACCCCTTAATTAATTAACACCACTGCTAGTACCAACTGCTGTGAGAA 1423
QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrSerLeuGlyAlaGlyProVal 200
Db 1424 GCCGCTGGGCAATCGGTTGCTATTTCACCTTACACCACTAGCCTGGGTGCTGGTCCCGTC 1483
QY 201 SerIleSerAlaValAlaValLeuAlaPro 210
Db 1484 TCTATTTCCGCGGTGCTGTTTATAGCCCCC 1513

RESULT 12
AR278920 1686-bp DNA linear PAT 10-APR-2003
LOCUS AR278920 Sequence 19 from patent US 6514690.
DEFINITION AR278920
ACCESSION AR278920
VERSION AR278920.1 GI:29713554
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1686)
AUTHORS Li, F., Hui, Z., Anderson, D.A., Logarini, S.A. and Torresi, J.
TITLE Immunoreactive antigens of Hepatitis E Virus
JOURNAL Patent: US 6514690-A 19 04-FEB-2003;
FEATURES Location/Qualifiers
source 1..1686
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 4,736-91 Length: 1686
Score: 1076.00 Matches: 210
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 6 Gaps: 0
US-10-089-292A-2 (1-213) x AR278920 (1-1686)

QY 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 20
Db 884 CAGCTGTTCTACTCTCGTCCCGCTCTCAGCAATGGCGAGCCGACTGTTAAGCTTTAT 943
QY 21 ThrSerValGluAsnAlaGlnAspLysGlyIleAlaIleProHisAspLeu 40
Db 944 ACATCTGAGAAATGCTCAGCAGATAAGGTAATGCAATCCCGATGACATCGACCTC 1003
QY 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
Db 1004 GGGAGTCTCGTGTAGTATTTCAGATTATGACACCAACATGACAGACCGACCGACA 1063
QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 80


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|||||
1064 CTTTCCCGAGCCCATCGGCCCTTTCTGCTCCAGCTATGATGCTTGGCTT 1123
QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
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1124 TCTCTCACCGCTGCGAGTAGACAGTCCAGTCCAGTCTTCCAGCGGCCAGTCTAT 1183
QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
|||||
1184 GTCTCTGACTCTGTGACCTTGGTTAATGTGCGACCGCGCGCGAGCGCTTCCCGGTCA 1243
QY 121 LeuAspTyrThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
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1244 CTCGACTGGACCAAGTACACTTGATGGTGGCCCTTCCACCATCCAGCAGTATTC 1303
QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTyrGluAlaGlyThrThr 160
|||||
1304 AAGACCTTCTTGTCTGCGCTGCGCGTAAAGTCTCTCTTTTGGAGGAGTACTACT 1363
QY 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuValGluAsn 180
|||||
1364 AAAGCGGGTACCTTATAATTAATATACACCACTGCTAGTACCACTGCTGTTGAGAT 1423
QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
|||||
1424 GCGCTGGGCATCGGGTGTCTATTTCCACTTACACCATAGCTGGTGGTGGTCCCGTTC 1483
QY 201 SerIleSerAlaValAlaValLeuAlaPro 210
|||||
1484 TCTATTTCGCGGTGCTGTTTTAGCCCC 1513

RESULT 13
HEVBCN6 1946 bp RNA linear VPL 17-NOV-1998
LOCUS Hepatitis E virus nonstructural polyprotein and structural protein
DEFINITION genes, partial cds; and unknown gene.
ACCESSION AF058684
VERSION AF058684.1 GI:3882959
KEYWORDS
SEGMENT
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1946)
Pina,S., Jofre,J., Emerson,S.U., Purcell,R.H. and Girones,R.
Characterization of a strain of infectious hepatitis E virus
isolated from sewage in an area where hepatitis E is not endemic
Appl. Environ. Microbiol. 64 (11), 4485-4488 (1998)
99043657
PUBMED 9797311
REFERENCE
2 (bases 1 to 1946)
Pina,S., Jofre,J., Shapiro,M., Emerson,S.U., Purcell,R.H. and
Girones,R.
Direct Submission
Submitted (09-APR-1998) Department of Microbiology, School of
Biology, University of Barcelona, Diagonal Avenue 645, Barcelona
08026, Spain
Location/Qualifiers
1. .1946
/organism="Hepatitis E virus"
/mol_type="genomic RNA"
/strain="BCN"
/db_xref="taxon.12461"
/country="Spain:Barcelona"
<1. .95
/notes="ORF1"
/codon_start=3
/product="nonstructural polyprotein"
/protein_id="AAC77805.1"
/db_xref="GI.3882967"
/translation="LQAVADGKAHFTESVKPVLDTNSILCRVE"
misc_feature <1. .92

/notes="Region: putative RNA-directed RNA polymerase"
92. .463
/notes="ORF3"
/codon_start=1
/product="unknown"
/protein_id="AAC77807.1"
/db_xref="GI.3882969"
/translations="MNMNSFAAPMGSRPCALGIFCCSSCFCLCCPRHRVSRILAAVV
GGAAPAVVGVGTGLILRPSQPIQTPTSPSPMSPRLPGLDLVFNPPDHPASPLGV
TRSPAPLPHVVDLPQLGPRR"
133. .>1946
/notes="ORF2"
/codon_start=1
/product="structural protein"
/protein_id="AAC77808.1"
/db_xref="GI.3882970"
/translation="MSRPULLFLMFLPMLPAPPQSQSSRRRRSGSGSGGFGWD
RVSDPPAIPIHTPNPAPDVTAAAGAGPRVQPARPLGSAMWDOARPAASRRRP
TTGAAPLTAFAHDTPVPDVSRRGAILRRQNLSTLSTSVATGTLNLYAAPL
SPLLPQDGTNTHIMATEASNYAQYVARATIRYRPLVPNAVGGYALISFWPOTTT
PTSDMNSITSDVRILOPGIASLIVIPSERLHYRNGRRSVETSGVQEEATSGLV
MLCTHSGPVSNSYNTPTVYTGALGLDPALELRLNLTGNTNTRVSRSTARHLRRG
ADGTAELTTTAATREMDLYFTSNNGVGEIGRGIATLFLNADTLGLGLPTLISAG
GQIFYSPVVSANGEPVTKLYTSVENAQDQKGIATPHDIDLGESRVVIQYDNOHQEOD
RPTSPAPSPFSLVRANDVLMLSLTAAEIQDSYSGSTGSPVYSDSVTLVNVATGAQ
AVARSLDWTKVTLDRPLSTIQOYSKTFVFLPLRGLKLSFWEAGTTKAGYPYNTITAS
DQLLVENAAHVRVAISTYTTSLGAGPVVISAVAVLAPHS"
133. .>1946
misc_feature
/notes="Region: putative capsid protein"

ORIGIN
Alignment Scores:
Pred. No.: 5,7e-91 Length: 1946
Score: 1076.00 Matches: 216
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 14 Gaps: 0
US-10-089-292A-2-(1-213) x HEVBCN6 (1-1946)
QY 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 20
DB 1312 CAGCTGTCTACTCCGTCCTGCTCAGCCAAATGCGGAGCGACTGTTAAGCTGAT 1371
QY 21 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 40
DB 1372 ACATCTGTAGAGATGCTCAGCAGGATAAGGATATCGCAATCCCGCATATATTCACCTC 1431
QY 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
DB 1432 GGAGAGTCTCGTGTGTTTATTCAGGATATATGATACCAACATGAACAGACCGCGCAGC 1491
QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTyrLeu 80
DB 1492 CCTTCTCAGCGCCCTCGCGCCCTTCTCTGTTCTTCGAGTAAATGATGCTTTGGCTC 1551
QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
DB 1552 TCTCTCAGCGCTGCGAGTATGACCACTATGCTTCTTCGACTGGCCAGTATAT 1611
QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
DB 1612 GTTCTGACTCTGTGACCTTGGTTAATGTGCGACCGCGCGCGAGCCCTTCCCGGTCC 1671
QY 121 LeuAspTyrThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
DB 1672 CTCGACTGGACCAAGTACACTTGACGCTGCCCTCTCTCCACCATCCAGCAGTACTCG 1731
QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTyrGluAlaGlyThrThr 160
DB 1732 AAGACCTTCTTGTCTGCGCTGCGCGCAAGCTCTCTTCTTGGAGGCGGCGCAACT 1791
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QY 161 LysAlaGlyTyrProTyrAsnTyrThrAlaSerAspGlnLeuValIleuAsn 180
 Db 1792 AAGCCGGGTACCCCTTAATTAATACACACCACTGCTAGCAGCACTGCTGTGAGAAAT 1851
 QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrSerLeuGlyValAlaGlyProVal 200
 Db 1852 GCCCGCGGACCGGGTGGCATCTCCACTTACACCACTAGCTGGGTGCTGGCCCGTC 1911
 QY 201 SerIleSerAlaValAlaValLeuAlaPro 210
 Db 1912 TCCATTTCTCGCGTTCCTAGCCCCC 1941
 RESULT 14
 LOCUS E17107 Hepatitis E virus ORF2. 1983 bp DNA linear PAT 28-JUL-1999
 DEFINITION Hepatitis E virus ORF2.
 ACCESSION E17107
 VERSION E17107.1 GI:5711790
 KEYWORDS JP 1998234383-A/3.
 SOURCE unidentified
 ORGANISM unidentified
 REFERENCE 1 (bases 1 to 1983)
 AUTHORS Takeda,N., Ri,T. and Miyamura,T.
 TITLE HEPATITIS E VIRUS HOLLOW PARTICLE, GENE ENCODING THE SAME AND PREPARATION OF RECOMBINATION VECTOR CONTAINING THE GENE AND UTILIZATION OF THE RECOMBINATION VECTOR
 JOURNAL Patent: JP 1998234383-A 3 08-SEP-1998;
 COMMENT DENKA SEIKEN CO LTD, KOKURITSU KANSENSHIYOU KENKYUSHO
 OS Hepatitis E virus
 PN JP 1998234383-A/3
 PD 08-SEP-1998
 PF 28-FEB-1997 JP 1997062445
 PI TAKEDA NAOKAZU, RI TENSEI, MIYAMURA TATSUO
 PC C12N15/09, C07K14/08, C12N5/10, C12P21/02;
 CC strandedness: Double;
 CC topology: Linear;
 FH Key Location/Qualifiers
 FT source 1..1983 /organism='Hepatitis E virus' FT CDS
 FT 1..1983 /product='structural protein'.
 FEATURES
 source Location/Qualifiers
 1..1983 /organism='unidentified'
 /mol_type='genomic DNA'
 /db_xref='taxon:32644'
 ORIGIN
 Alignment Scores: 5,85e-91 Length: 1983
 Pred. No.: 1076.00 Matches: 210
 Score: 1076.00 Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 98.26% Gaps: 0
 DB: 6
 US-10-089-292A-2 (1-213) x E17107 (1-1983)
 QY 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValIleAspLeuTyr 20
 Db 1180 CAGCTGTTCTACTCCGTCCTCGGTGCTCGGCAATGGCAGCCGACTGTTAAGTTGAT 1239
 QY 21 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 40
 Db 1240 ACATCTGTAGAAATGCTCAGCAGGATAAGGTATTGCAATCCCGCATGACATTCACCTC 1299
 QY 41 GlyGluSerArgValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
 Db 1300 GGAGAATCTCGTGTGTTATTTCAGATTATGACACCAACATGAACAGATCGGCCGACG 1359
 QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 80

Db 1360 CCTTCTCAGGCCCATCGGCCCTTTCTCTGCTCTTCGAGCTAATGATGCTTTGGCTC 1419
 QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
 Db 1420 TCTCTCACCCTGCGAGTATGACAGTCCACTTATGGCTCTTCGACTGGCCAGTTAT 1479
 QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
 Db 1480 GTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGCGCGAGCGCTTGCCTGGTCG 1539
 QY 121 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
 Db 1540 CTCGATTGGACCAAGTTCACACTTTCGCGTCCGCCCTCTCCCATCCAGCAGTACTCG 1599
 QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 160
 Db 1600 AAGACCTTCTTTGTCTCGCGCTCCGCGGTAAAGCTCTCTTTCTGGAGGAGGCACAACT 1659
 QY 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuValGluAsn 180
 Db 1660 AAGCCGGGTACCTTATATTAACACCACTGCTAGCAGCACTGCTTGTGAGAAAT 1719
 QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
 Db 1720 GCCCGCGGACCGCGTGCCTATTTCACCTTACACCACTAGCTGGGTGCTGGTCCCGTC 1779
 QY 201 SerIleSerAlaValAlaValLeuAlaPro 210
 Db 1780 TCCATCTCGCGTGTGCTGTTTAGCCCCC 1809
 RESULT 15
 LOCUS I73139 1983 bp DNA linear PAT 03-APR-1998
 DEFINITION Sequence 1 from patent-US-5686239.
 ACCESSION I73139
 VERSION I73139.1 GI:3009278
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 1983)
 AUTHORS Reyes,G.R., Tam,A.W. and Varbough,P.O.
 TITLE Hepatitis E virus peptides and methods
 JOURNAL Patent: US 5686239-A 1 11-NOV-1997;
 FEATURES Location/Qualifiers
 source 1..1983
 /organism='unknown'
 /mol_type='unassigned DNA'
 ORIGIN
 Alignment Scores: 5,85e-91 Length: 1983
 Pred. No.: 1076.00 Matches: 210
 Score: 1076.00 Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 98.26% Gaps: 0
 DB: 6
 US-10-089-292A-2 (1-213) x I73139 (1-1983)
 QY 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValIleAspLeuTyr 20
 Db 1180 CAGCTGTTCTACTCCGTCCTCGGTGCTCGGCAATGGCAGCCGACTGTTAAGTTGAT 1239
 QY 21 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 40
 Db 1240 ACATCTGTAGAAATGCTCAGCAGGATAAGGTATTGCAATCCCGCATGACATTCACCTC 1299
 QY 41 GlyGluSerArgValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
 Db 1300 GGAGAATCTCGTGTGTTATTTCAGATTATGACACCAACATGAACAGATCGGCCGACG 1359

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QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 80
Db 1360 CCTTCTCCAGCCCATCGCGCCTTCTCTGCTTCGAGCTAATGATGTGCTTTGGCTC 1419
QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
Db 1420 TCTCTCACCGCTGCCGAGTATACCACTTATGCTCTTCGACTGGCCCAAGTTTAT 1479
QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyValaGlnAlaValAlaArgSer 120
Db 1480 GTTTCGTGACTCTGTGACCTTGGTTAATGTTGGACCGCGCGCAGGCCCTTCCCGGTG 1539
QY 121 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
Db 1540 CTCGATTGGACCAAGGTCACACTTGACGGTCGCCCTCTCCACCATCCAGCAGTACTCG 1599
QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 160
Db 1600 AAGACCTTCTTTGCTGCTGCCGCTCCGCGGTAAAGCTCTCTTTCTGGGAGGCGGCACAACT 1659
QY 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 180
Db 1660 AAAGCGGGTACCTTATATATTAACACCACTGCTAGCAGCAACTGCTTGTTCAGAGAT 1719
QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
Db 1720 GCCGCGGGGACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTC 1779
QY 201 SerIleSerAlaValAlaValLeuAlaPro 210
Db 1780 TCCATTCTCGCGTTGCCGTTTTCAGCCCC 1809
```

Search completed: October 28, 2004, 11:15:54
Job time : 2721 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 28, 2004, 09:42:54 ; Search time 330 Seconds
(without alignments)
3388.263 Million cell updates/sec

Title: US-10-089-292A-2
Perfect score: 1095
Sequence: 1 QLFYRVPVSGANGPTVKLY.....SLGAGPVSISSAVLAPPPR 213

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US10089292/runat_27102004_153927_10148/app_query.fasta_1.391
-DB=N_Geneseq_23Sep04 -QPMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPECL=0
-LOOPEXT=0 -UNIT5=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10089292 @CGN 1 1 352 @runat_27102004_153927_10148 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6
-FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1095	100.0	810	4 AAS01434	Aas01434 Hepatitis
2	1095	100.0	1989	6 ABL60054	Abi60054 Hepatitis
3	1095	100.0	1989	10 ADB97809	Adb97809 HEV relat
4	1076	98.3	984	2 AAT27111	Aat27111 Hepatitis
5	1076	98.3	984	2 AAT96965	Aat96965 Hepatitis
6	1076	98.3	1647	2 AAT27109	Aat27109 Hepatitis

7	1076	98.3	1647	2 AAV61686	Aav61686 Hepatitis
8	1076	98.3	1983	2 AAT96959	Aat96959 Hepatitis
9	1076	98.3	1983	2 AAV61688	Aav61688 Hepatitis
10	1076	98.3	1984	2 AAQ86592	Aaq86592 Hepatitis
11	1076	98.3	1990	6 ABL60053	Abi60053 Hepatitis
12	1076	98.3	1990	10 ADB97808	Adb97808 HEV ORF2
13	1076	98.3	2049	2 AAT27107	Aat27107 Hepatitis
14	1076	98.3	2054	4 AAS01448	Aas01448 Hepatitis
15	1076	98.3	2094	2 AAQ47129	Aaq47129 HEV thirid
16	1076	98.3	2094	2 AAQ46813	Aaq46813 Burma str
17	1076	98.3	7158	2 AAT27394	Aat27394 Hepatitis
18	1076	98.3	7158	2 AAQ45197	Aaq45197 HEV strai
19	1076	98.3	7168	2 AAV71604	Aav71604 Hepatitis
20	1076	98.3	7194	2 AAV61690	Aav61690 Hepatitis
21	1076	98.3	7195	2 AAV66321	Aav66321 ET-NANB (
22	1076	98.3	7195	2 AAV54729	Aav54729 DNA seque
23	1076	98.3	7195	3 AAA99259	Aaa99259 Hepatitis
24	1076	98.3	7195	4 AAF83495	Aaf83495 ET-NANB v
25	1076	98.3	7195	6 AAL50386	Aal50386 Hepatitis
26	1076	98.3	7204	9 ADA50062	Ada50062 SK-HEV-3
27	1076	98.3	7204	9 ADA50065	Ada50065 Hepatitis
28	1076	98.3	7204	9 ADA50064	Ada50064 Hepatitis
29	1076	98.3	7204	9 ADA50063	Ada50063 SK-HEV-2
30	1073	98.0	7195	2 AAQ14412	Aaq14412 Forward s
31	1067	97.4	7195	10 ADD24374	Add24374 Hepatitis
32	1051	96.0	7099	5 ADH13466	Adh13466 Hepatitis
33	1051	96.0	7194	5 ADH13469	Adh13469 Hepatitis
34	1043	95.3	984	2 AAT27112	Aat27112 Hepatitis
35	1043	95.3	984	2 AAT96966	Aat96966 Hepatitis
36	1043	95.3	1647	2 AAT27110	Aat27110 Hepatitis
37	1043	95.3	1980	2 AAT96960	Aat96960 Hepatitis
38	1043	95.3	2058	2 AAT27108	Aat27108 Hepatitis
39	1043	95.3	2100	2 AAQ47130	Aaq47130 HEV thirid
40	1043	95.3	7171	2 AAQ14413	Aaq14413 Composite
41	1043	95.3	7171	2 AAV66322	Aav66322 ET-NANB (
42	1043	95.3	7171	2 AAV54730	Aav54730 Composite
43	1043	95.3	7171	3 AAA99260	Aaa99260 Hepatitis
44	1043	95.3	7171	4 AAF83496	Aaf83496 Mexican s
45	1043	95.3	7171	6 AAL50387	Aal50387 Hepatitis

ALIGNMENTS

RESULT 1
AAS01434
ID AAS01434 standard; cDNA; 810 BP.
XX
AC AAS01434;
XX
DT 18-JUL-2001 (first entry)
XX Hepatitis E virus (HEV) E2 cDNA fragment derived from ORF2.
XX Hepatitis E virus; HEV; E2; PE2; ORF2; immunoreactive viral peptide;
KW antigenic activity; viral infection; mutant; ss.
XX Hepatitis E virus; Chinese strain D11092.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..810
FT /tag= b
FT /note= "Corresponds to residues 1180-1990 of ORF2"
FT CDS 1..642
FT /tag= a
FT /partial
FT /product= "pE2 peptide"
FT /note= "Specifically claimed. This sequence lacks a start
FT codon"
FT mutation replace(631..632, CAC)
XX
PN WO200122916-A2.

XX 05-APR-2001.
 XX 28-SEP-2000; 2000WO-1B001393.
 XX 30-SEP-1999; 99CA-02283538.
 XX (UYHK-) UNIV HONG KONG.
 XX Ng MH, Im S, Zhang J;
 XX WPI; 2001-266109/27.
 DR P-PSDB; AAU00496.
 PT New immunoreactive peptide pE2, cloned from the genome of a Chinese
 PT strain of hepatitis E virus (HEV), for detecting and diagnosing HEV
 PT infection and for use as a vaccine for prevention of the viral infection
 PT in humans.
 XX
 PS Claim 5; Fig 2B-2D; 101pp; English.
 CC The present sequence for hepatitis E virus (HEV) E2 cDNA fragment encodes
 CC for a novel peptide, pE2 which is cloned from ORF2 (AA501448) of the HEV
 CC Chinese strain D11092 genome. During the cloning of the E2 fragment a
 CC single base deletion (presumed to be a PCR amplification error) at
 CC position 1811 of ORF2 resulted in a frame shift causing the premature
 CC termination at a new stop codon at position 1820-1822, and giving rise to
 CC a smaller peptide, pE2. Peptide pE2 is a highly immunoreactive viral
 CC peptide which can be used in the development of diagnostic methods for
 CC the detection of HEV. Peptide pE2 which has antigenic activity is also
 CC useful as a vaccine for immunising an individual against infection from
 CC HEV and for determining the presence of HEV antibodies in a biological
 CC test sample such as human blood serum or plasma for detection and
 CC diagnosis of HEV infection. An antibody against pE2 is useful for
 CC detecting an HEV particle, in a biological test sample. The use of
 CC recombinant peptides such as pE2 peptide have advantage over the prior
 CC art of using live intact virus particles by avoiding the potential risk
 CC of infectivity. The ORF3 (AA501449) of HEV Chinese strain D11092 is used
 CC to clone a cDNA fragment E3 (AA5001450) which encodes pE3 peptide
 XX
 SQ Sequence 810 BP; 150 A; 249 C; 192 G; 219 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.09e-103 Length: 810
 Score: 1095.00 Matches: 213
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-10-089-292A-2 (1-213) x AA501434 (1-810)

QY 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValIysLeuTyr 20
 DB 1 CAGCTGTTCTACTCTCGTCCGCTCGTCTCAGCAATGCGGACCGACTGTTAAGCTTAT 60
 QY 21 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 40
 DB 61 ACATCTGTAGAGATGCTCAGCAGATAGAGGATGTCATCCCGATGACATCGACCTC 120
 QY 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
 DB 121 CGGGAGTCTCGTGTAGTTATTTCAGGATTATGACCAACATGAGCAGGACCGACGACA 180
 QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 80
 DB 181 CCTTCCCAAGCCCAATCGCGCCCTTTCTGCTCCCGAGCTAATGATGTCTTGGCTT 240
 QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
 DB 241 TCTCTCAGCGCTGCCGAGTATGACCACTTACGAGTCTTCGACCGGCGCCAGTCTAT 300
 QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120

DB 301 GTCTCTGACTCTGTGACCTTGGTTAATGTGGAGCCGCGCGCAGGCCGTTGCCCGGTCA 360
 QY 121 LeuAspTyrThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
 DB 361 CTCGACTGAGCAAGGTACACTTGTATGTCGCCCTTTTCACCATCCAGCAGTATTCA 420
 QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTyrGluAlaGlyThrThr 160
 DB 421 AAGACTCTTCTTGTCTGCGGCTCGCGGTAAGCTCTCTCTTTGGAGGACGAGTACTACT 480
 QY 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuValGluAsn 180
 DB 481 AAAGCCGGGTACCTTATAATTAACACCACTGCTAGTGACCACTGCTCGTTGAGAAT 540
 QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
 DB 541 GCCGCTGGGCAATCGGGTTGCTATTTCACCTTACACCACTAGCTGGGTCTGGTCCCCTC 600
 QY 201 SerIleSerAlaValAlaValLeuAlaProProAlaG 213
 DB 601 TCTATTTCGGGGTGTGCTTTTAGCCCCCTCCGCGC 639
 RESULT 2
 ID ABL60054
 AC ABL60054 standard; DNA; 1989 BP.
 XX ABL60054;
 XX 16-AUG-2002 (first entry)
 XX Hepatitis E virus ORF-2 DNA #2.
 XX Hepatitis E virus; ORF-2; HEV; virucide; immunisation; gene; ds.
 XX Hepatitis E virus.
 XX WO200240681-A1.
 XX 23-MAY-2002.
 XX 30-SEP-2001; 2001WO-CN001469.
 XX 30-SEP-2000; 2000CN-00130634.
 XX (YANG-) YANG SHENG TANG CO LTD.
 XX Xia N, Zhang J, Li S, Ge S, Gu Y, He Z;
 WPI; 2002-427096/45.
 PT Polypeptide fragments of hepatitis E virus (HEV) for vaccine compositions
 PT and diagnosis in preventing and treating HEV infection.
 XX Example 1; Page 83-84; 91pp; Chinese.
 CC The sequence encodes hepatitis E virus (HEV) ORF-2 polypeptide. The
 CC invention relates to novel n-mer polypeptides comprising amino acids of
 CC ORF-2 of HEV where n = 2-180. The polypeptides of the invention have
 CC virucide activity. The polypeptide of HEV, its fragments, and chimeric
 CC proteins, are useful for vaccine compositions and diagnosis in preventing
 CC and treating HEV infection by immunisation, which may also be applied in
 CC the diagnosis of HEV infection
 XX
 SQ Sequence 1989 BP; 347 A; 666 C; 481 G; 495 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3.58e-103 Length: 1989
 Score: 1095.00 Matches: 213
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-089-292A-2 (1-213) x ABL60054 (1-1989)

Qy 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 20
Db 1180 CAGCTGTTCTACTCTCGTCCGCTGCTCTCAGCAATGCGAGCGACTGTTAAGCTTTAT 1239
Qy 21 ThrSerValGluAsnAlaGlnAspLysGlyLeuAlaIleProHisAspIleAspLeu 40
Db 1240 ACATCTGTAGAGATGCTCAGCAGGATAAGGTTATTCGAATCCCGCATGACATCGACCTC 1299
Qy 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
Db 1300 GGGAGTCTCGTGTAGTTATTCAGATTATGACACCAACATGACAGACCGACCGACA 1359
Qy 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 80
Db 1360 CTTTCCCGCAGCCCATCGGCCCTTTCTGCTCCGAGCTAATGATGTCTTTGGCTT 1419
Qy 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
Db 1420 TCTCTACCGCTGCGAGTATGACAGTCCACTTACGGCTCTTCGACCGGCCAGTCTAT 1479
Qy 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
Db 1480 GTCTCTGACTCTGTGACCTTGTGTTAATGTTGCGACCGCGCGAGCGCTTGCCCGGTCA 1539
Qy 121 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnTyrSer 140
Db 1540 CTCGACTGACCAAGTTCACACTTGATGTCGCCCTTTCCACCATCGACAGATTATCA 1599
Qy 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 160
Db 1600 AAGACCTTCTTTGTCTGCTCGCGTAAAGCTCTCTCTTTGGGAGGCGAGTACTACT 1659
Qy 161 LysAlaGlyTyrProTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 180
Db 1660 AAGCCGGGTACCTTATAATTAATTAACACCACTGCTAGTACCACTGCTGTTGAGAA 1719
Qy 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
Db 1720 GCCGCTGGGCATCGGTTGCTATTTCCACTTACACCATAGCTGGGTGCTGGTCCCGTC 1779
Qy 201 SerLeuSerAlaValAlaValLeuAlaProProArg 213
Db 1780 TCTATTTCGGCGGTGCTGTTTATAGCCCCCTCGCGC 1818

RESULT 3

ADB97809
ID ADB97809 standard; DNA; 1989 BP.

XX AC ADB97809;

XX DT 04-DEC-2003 (first entry)

XX DE HEV related DNA #SEQ ID 3.

XX KW Hepatitis E virus; HEV; virucide; vaccine; monoclonal antibody; NE2;
XX KW infection; ds.

XX OS Unidentified.

XX PN WO2003040187-A1.

XX PD 15-MAY-2003.

XX XX 08-NOV-2002; 2002WO-CN000797.

XX XX 08-NOV-2001; 2001CN-00134643.

XX XX (YANG-) YANG SHENG TANG CO LTD.

XX PI Xia N, Zhang J, Gu Y, Li S, Ge S, He Z;

XX WPI; 2003-441530/41.

XX Hepatitis E virus monoclonal antibodies and their active fragments, for
PT use in diagnosis and developing remedies e.g. vaccines for preventing or
PT treating hepatitis E virus infection.

XX Example 1; Page 133-135; 165pp; Chinese.

XX The invention relates to a monoclonal antibody that binds specifically to
CC hepatitis E virus open-reading frame (ORF) 2. Also disclosed are
CC nucleotide sequences encoding the heavy-chain and/or light-chain variable
CC region of their degeneration sequences. The monoclonal antibody is
CC selected from anti-HEV monoclonal antibody 8C11 secreted by hybridoma
CC CTCC-C200116, anti-HEV monoclonal antibody 13D8 secreted by hybridoma
CC CTCC-C200114, anti-HEV monoclonal antibody 8H3 secreted by hybridoma
CC CTCC-C200117, and anti-HEV monoclonal antibody 16D7 secreted by
CC hybridoma CTCC-C200114. The monoclonal antibodies and their active
CC fragments are useful in diagnosis and developing remedies e.g. vaccines
CC for preventing or treating hepatitis E virus infection. From the whole
CC HEV gene obtained in patients, the HEV ORF fragment was prepared by using
CC the method of Aye et al. The polypeptide NE2 was then expressed and
CC isolated after biotechnological manipulations, which was characterised.
CC Its analogs were also produced for immunising mice and construction of
CC hybridomas. Tests were carried out to confirm usefulness of such
CC polypeptides and monoclonal antibodies. The current sequence represents a
CC HEV related DNA.

XX SQ Sequence 1989 BP; 347 A; 666 C; 481 G; 495 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.58e-103 Length: 1989
Score: 1095.00 Matches: 213
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-089-292A-2 (1-213) x ADB97809 (1-1989)

Qy 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 20
Db 1180 CAGCTGTTCTACTCTCGTCCGCTGCTCTCAGCAATGCGAGCGACTGTTAAGCTTTAT 1239
Qy 21 ThrSerValGluAsnAlaGlnAspLysGlyLeuAlaIleProHisAspIleAspLeu 40
Db 1240 ACATCTGTAGAGATGCTCAGCAGGATAAGGTTATTCGAATCCCGCATGACATCGACCTC 1299
Qy 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
Db 1300 GGGAGTCTCGTGTAGTTATTCAGATTATGACACCAACATGACAGACCGACCGACA 1359
Qy 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 80
Db 1360 CTTTCCCGCAGCCCATCGGCCCTTTCTGCTCCGAGCTAATGATGTCTTTGGCTT 1419
Qy 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
Db 1420 TCTCTACCGCTGCGAGTATGACAGTCCACTTACGGCTCTTCGACCGGCCAGTCTAT 1479
Qy 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
Db 1480 GTCTCTGACTCTGTGACCTTGTGTTAATGTTGCGACCGCGCGAGCGCTTGCCCGGTCA 1539
Qy 121 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnTyrSer 140
Db 1540 CTCGACTGACCAAGTTCACACTTGATGTCGCCCTTTCCACCATCGACAGATTATCA 1599
Qy 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 160
Db 1600 AAGACCTTCTTTGTCTGCTCGCGTAAAGCTCTCTCTTTGGGAGGCGAGTACTACT 1659
Qy 161 LysAlaGlyTyrProTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 180

PR 05-APR-1990; 90US-00505888.
 PR 05-APR-1991; 91US-00681078.
 PR 17-JAN-1992; 92US-00822335.
 PR 20-APR-1992; 92US-00870985.
 PR 01-MAY-1992; 92US-00876941.
 XX (GENE-) GENELABS TECHNOLOGIES INC.
 XX
 PI Tam AW, Reyes GR, Yarbough PO;
 XX
 DR P-PSDB; AAW35820.
 XX
 XX Diagnosis of hepatitis E virus Burma and Mexico strain infection - by
 PT immunoassay with hepatitis E virus peptide antigens.
 XX
 PS Disclosure; Col 29-32; 36pp; English.
 XX
 CC A method has been developed for detecting hepatitis E virus (HEV)
 CC antibodies (Ab). The method comprises: (a) reacting a serum sample with a
 CC HEV peptide antigen; and (b) examining the peptide for the presence of
 CC bound Ab, where the presence of bound Ab indicates the presence of HEV
 CC Ab. The present sequence encodes a specifically claimed HEV peptide
 CC antigen. The method can be used to diagnose infection with the
 CC enterically transmitted non-A/non-B viral hepatitis agent HEV,
 CC specifically the HEV Burma and Mexico strains. (Updated on 25-MAR-2003 to
 CC correct PF field.) (Updated on 17-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 984 BP; 180 A; 300 C; 246 G; 258 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.3e-101 Length: 984
 Score: 1076.00 Matches: 210
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.26% Indels: 0
 DB: 2 Gaps: 0
 US-10-089-292A-2 (1-213) x AAT96965 (1-984)
 QY 1 GlnLeuPheTyrSerArgProValValSerAlaAenGlyGluProThrValLysLeuTyr 20
 DB 181 CAGCTGTTCTACTCCGTCCTCGTGTCTCAGCAATGGCGAGCCGACGTGAAGTTGAT 240
 QY 21 ThrSerValGluAenAlaGlnAspLysGlyLleAlaIleProHisAspIleAspLeu 40
 DB 241 ACATCTGTAGAGATGCTCAGCAGGATGAAGGTATTGCAATCCCGCATGACATTGACCTC 300
 QY 41 GlyGluSerArgValValIleGlnAspTyrAspAenGlnHisGluGlnAspArgProThr 60
 DB 301 GGAGAATCTCGTGTGTATTTCAGGATTATGATAACCAACATGAACAAGATCGGCCGACG 360
 QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAenAspValLeuTrpLeu 80
 DB 361 CTTCTCCAGCCCCATCGGCCCTTCTCTGTCCTTCGAGCTAATGATGCTTTGGCTC 420
 QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerThrGlyProValTyr 100
 DB 421 TCTCTCACCGCTGCGAGATGATGACCCAGTCCACTTATGCTCTTCGACTGGCCAGTTAT 480
 QY 101 ValSerAspSerValThrLeuValAenValAlaThrGlyAlaGlnAlaValAlaArgSer 120
 DB 481 GTTCTTGACTCTGTGACCTTGGTTAATGTTGCGACCGCGCGAGCGGTTGCCCGTGC 540
 QY 121 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnThrSer 140
 DB 541 CTCGATTGACCAAGGTACACTTCAGCGTCCGCCCTCTCCACCATCCAGCAGTACTCG 600
 QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 160
 DB 601 AAGACTTCTTGTCTCGCGCTCCGCGTGAAGTCTCTTCTTGGGAGGAGGACCAACT 660
 QY 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAen 180

Db 661 AAAGCCGGTACCTTATAATTAAACCACTGCTAGCACCACTGCTTGTCCAGAA 720
 QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
 DB 721 GCCGCCGGCACCGGTGCTATTTCACCTTACCACTAGCTGCTGGTGGTCCCGTC 780
 QY 201 SerIleSerAlaValAlaValLeuAlaPro 210
 DB 781 TCCATTCTCGCGTTGCCGTTTATAGCCCC 810
 RESULT 6
 AAT27109
 ID AAT27109 standard; DNA: 1647 BP;
 XX
 AC AAT27109;
 XX
 DT 16-OCT-2003 (revised)
 DT 06-AUG-1996 (first entry)
 XX
 DE Hepatitis E virus (Burma strain) 62K antigen DNA.
 XX
 DE HEV, enterically-transmitted non-A/non-B hepatitis virus; vaccine;
 KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
 KW capsid; db.
 XX
 OS Hepatitis E virus; Burma strain.
 XX
 PN WO9612807-A2.
 XX
 PD 02-MAY-1996.
 XX
 PF 23-OCT-1995; 95WO-US013703.
 XX
 PR 24-OCT-1994; 94US-00327952.
 PR 13-OCT-1995; 95US-00542634.
 XX
 PA (GENE-) GENELABS TECHNOLOGIES INC.
 XX
 PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;
 XX
 DR WPI, 1996-230608/23.
 DR P-PSDB; AAR96090.
 XX
 PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
 PS diagnostic reagents for determining HEV infection and in vaccines.
 XX
 PS Disclosure; Page 72-73; 125pp; English.
 XX
 CC A DNA sequence (AAT27109) codes for 62K antigen (AAR96091) comprising the
 CC C-terminal 549 amino acids of hepatitis E virus (HEV) Burma strain capsid
 CC protein (AAR96089). It is obt'd. by PCR amplification of HEV Burma ORF-2
 CC (AAT27107) from pBET1 plasmid. The amplified fragment is inserted into
 CC vector pGEX for prodn. 62K in E. coli cells. Expression of full-length
 CC ORF-2 in Sf9 insect cells using a baculovirus system also results in
 CC prodn. of 62K antigen (see also AAR96101 and AAR96103). 62K represents an
 CC improved antigen, in comparison to bacterial expressed proteins, for use
 CC in HEV diagnostic assays, and also has excellent immunogenic properties.
 CC (Updated on 16-OCT-2003 to standardise OS field)
 SQ Sequence 1647 BP; 302 A; 533 C; 391 G; 421 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2.58e-101 Length: 1647
 Score: 1076.00 Matches: 210
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.26% Indels: 0
 DB: 2 Gaps: 0
 US-10-089-292A-2 (1-213) x AAT27109 (1-1647)
 QY 1 GlnLeuPheTyrSerArgProValValSerAlaAenGlyGluProThrValLysLeuTyr 20

```
Db 847 CAGCTGTTCTACTCCGTCCTCTCAGCAATGCGGCGGACTGTTAAGTTGAT 906
QY 21 ThrSerValGluAsnAlaGlnAspLysGlyLeuAlaIleProHisAspIleAspLeu 40
Db 907 ACATCTGTAGAGATGCTCAGCAGGATAAGGTTATTGCAATCCCGCATGACATTGACCTC 966
QY 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
Db 967 GGAGAATCTCGTGTGTTATTTCAGGATTATGATAACCAACATGAACAAGATCGGCCGACG 1026
QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 80
Db 1027 CTTTCTCAGCCCCATCGGCCCTTCTCTGCTCTCAGCTAATGATGCTTTGGCTC 1086
QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrGlySerSerThrGlyProValTyr 100
Db 1087 TCTCTCAGCGCTGCGGAGTATGACGATGACCTTATGCTCTTCGACTGGCCGACGTTTAT 1146
QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
Db 1147 GTTCTCGACTCTGTGACCTTGTGTTAATGTTGCGACCGCGCGGCGGCTTGGCGGTCG 1206
QY 121 LeuAspTyrThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
Db 1207 CTCGATTGACCAAGGTGACACTTGACGGTCCGCCCTCTCCACCATCCAGCAGTACTCG 1266
QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 160
Db 1267 AAGACCTTCTTGTCTCGCTCGGCTCGCGGTAAGCTCTCTTCTGGGAGGACGACAACT 1326
QY 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 180
Db 1327 AAAGCCGGGTACCTTATTAATTAACACCATGCTGAGGACCAACTGCTTGTCCGGAAT 1386
QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
Db 1387 GCGCGCGGACCGGGTCTGCTATTTCCACTTACACCATAGCTGGGTCTGGTCCCGTC 1446
```

RESULT 7

```
AAV61686
ID AAV61686 standard; DNA; 1647 BP.
XX
AC AAV61686;
XX
DT 03-DEC-1998 (first entry)
DE Hepatitis E virus hollow particle protein ORF2 DNA.
XX
KW Hollow particle protein; virus; antibody; detection; immunoassay;
KW infection; ss.
XX
OS Hepatitis virus.
XX
FH Key Location/Qualifiers
FT CDS 1..1647
FT FT /*tag= a
FT FT /product= "hollow particle protein"
FT FT /note= "No start codon given for ORF2"
XX
FN JF10234393-A.
XX
PD 08-SEP-1998.
XX
PF 28-FEB-1997; 97JP-00062445.
XX
PR 28-FEB-1997; 97JP-00062445.
XX
PA (DENK-) DENKA SEIKEN KK.
```

(KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.

WPI: 1998-535037/46.

P-PSDB; AAW76367.

Hepatitis E virus hollow particle poly-peptide(s) and nucleic acids encoding it - useful for more accurate detection of HEV in samples, using immuno-assays and nucleic acid hybridisation.

Claim 1; Page 15-17; 29pp; Japanese.

This sequence encodes a Hepatitis E viral hollow particle protein described as ORF2. This polypeptide can be used to raise antibodies to detect HEV infection in samples, e.g. by immuno-assay based techniques, and the nucleic acid can be used for the same in nucleic acid hybridisation assays. The polypeptide and nucleic acid allow more accurate detection of HEV than previously possible

Sequence 1647 BP; 303 A; 535 C; 390 G; 419 T; 0 U; 0 Other;

Alignment Scores:

Alignment No.:	2,58e-101	Length:	1647
Score:	1076.00	Matches:	210
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	98.26%	Indels:	0
DB:	2	Gaps:	0

US-10-089-292A-2 (1-213) X AAV61686 (1-1647)

```
QY 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 20
Db 847 CAGCTGTTCTACTCCGTCCTCTCAGCAATGCGGCGGACTGTTAAGTTGAT 906
QY 21 ThrSerValGluAsnAlaGlnAspLysGlyLeuAlaIleProHisAspIleAspLeu 40
Db 907 ACATCTGTAGAGATGCTCAGCAGGATAAGGTTATTGCAATCCCGCATGACATTGACCTC 966
QY 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
Db 967 GGAGAATCTCGTGTGTTAATGTTGCGACCGCGGTAAGCTCTCTTCTGGGAGGACGACAACT 1026
QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 80
Db 1027 CTTTCTCAGCCCCATCGGCCCTTCTCTGCTCTCAGCTAATGATGCTTTGGCTC 1086
QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
Db 1087 TCTCTCAGCGCTGCGGAGTATGACGATGACCTTATGCTCTTCGACTGGCCGACGTTTAT 1146
QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
Db 1147 GTTCTCGACTCTGTGACCTTGTGTTAATGTTGCGACCGCGGCGGCTTGGCGGTCG 1206
QY 121 LeuAspTyrThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
Db 1207 CTCGATTGACCAAGGTGACACTTGACGGTCCGCCCTCTCCACCATCCAGCAGTACTCG 1266
QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 160
Db 1267 AAGACCTTCTTGTCTCGCTCGGCTCGCGGTAAGCTCTCTTCTGGGAGGACGACAACT 1326
QY 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 180
Db 1327 AAAGCCGGGTACCTTATTAATTAACACCATGCTGAGGACCAACTGCTTGTCCGGAAT 1386
QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
Db 1387 GCGCGCGGACCGGGTCTGCTATTTCCACTTACACCATAGCTGGGTCTGGTCCCGTC 1446
QY 201 SerIleSerAlaValAlaValLeuAlaPro 210
Db 1447 TCCATTCTGCGGTTCGCCGCTTTTAGCCCCC 1476
```



```
RESULT 8
AAT96959
ID AAT96959 standard; DNA; 1983 BP.
XX AC AAT96959;
XX DT 17-OCT-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 26-FEB-1998 (first entry)
XX DE Hepatitis E virus Burma strain ORF2.
XX KW Hepatitis E virus; Burma; Mexico; immunoassay; peptide antigen; antibody;
XX KW diagnosis; HEV; ds.
XX OS Hepatitis E virus; - Burma strain.
XX FH Key Location/Qualifiers
XX FT CDS 1..1983
XX FT FT /*tag= a
XX FT FT /product= "ORF2_protein"
XX PN US5686239-A.
XX XX
XX PD 11-NOV-1997.
XX PF 09-MAY-1994; 94US-00240049.
XX PR 17-JUN-1988; 88US-00208997.
XX PR 11-APR-1989; 89US-00336672.
XX PR 16-JUN-1989; 89US-00367486.
XX PR 13-OCT-1989; 89US-00420921.
XX PR 05-APR-1990; 90US-00505888.
XX PR 05-APR-1991; 91US-00681078.
XX PR 17-JAN-1992; 92US-00822335.
XX PR 20-APR-1992; 92US-00870985.
XX PR 01-MAY-1992; 92US-00876941.
XX PA (GENE-) GENELABS TECHNOLOGIES INC.
XX PI Tam AW, Reyes GR, Yarbough PO;
XX WPI; 1997-558132/51.
XX P-PSDB; AAW35826.
XX PT Diagnosis of hepatitis E virus Burma and Mexico strain infection - by
XX PT immunoassay with hepatitis E virus peptide antigens.
XX PS Disclosure; Col 23-24; 36pp; English.
XX CC A method has been developed for detecting hepatitis E virus (HEV)
XX CC antibodies (Ab). The method comprises: (a) reacting a serum sample with a
XX CC HEV peptide antigen; and (b) examining the peptide for the presence of
XX CC bound Ab, where the presence of bound Ab indicates the presence of HEV
XX CC Ab. The present sequence encodes the protein from the open reading frame,
XX CC ORF2, from HEV Burma strain. The method can be used to diagnose infection
XX CC with the enterically transmitted non-A/non-B viral hepatitis agent HEV,
XX CC specifically the HEV Burma and Mexico strains. (Updated on 25-MAR-2003 to
XX CC correct PF field.) (Updated on 17-OCT-2003 to standardise OS field)
XX SQ Sequence 1983 BP; 340 A; 665 C; 486 G; 492 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 3 29e-101 Length: 1983
Score: 1076.00 Matches: 210
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 2 Gaps: 0
US-10-089-292A-2 (1-213) x AAT96959 (1-1983)
Qy 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValIysLeuTyr 20
Db 1180 CAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTAT 1239
Qy 21 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 40
Db 1240 ACATCTGTAGAGAAATGCTCAGCAGGATTAAGGTATTGCAATCCCGCATGACATTGACCTC 1299
Qy 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
Db 1300 GGAGAATCTCGTGTGGTTATTTCAGGATTATGATTAACCAACATGAACAAGATCGGCCGACG 1359
Qy 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 80
Db 1360 CTTTCTCCAGCCCCATCGGCCCTTTCTGTGCTCTGAGCTAATGATGTGTTTGGCTC 1419
Qy 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
Db 1420 TCTCTCACCCTGCGAGTATGACCACTTATGGCTCTTCGACTGGCCAGTTTAT 1479
Qy 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
Db 1480 GTTTCCTGACTCTGTGACCTTGGTTAATGTTGCGACCGCGCGCAGCGCTTGCCTGGTTCG 1539
Qy 121 LeuAspTrpThrIysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
Db 1540 CTCGATTGGACCAAGGTACACTTTGACGGTCCGCCCTCTCCACCATCCAGCAGTACTCG 1599
Qy 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTyrGluAlaGlyThrThr 160
Db 1600 AAGACCTTCTTGTCTGCTCGCGCTCCGCGGTAAAGCTCTCTTCTGGAGGAGGACCAACT 1659
Qy 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluLeu 180
Db 1660 AAAGCCGGTACCTTATTAATTAAACACCACTGCTAGCGACCAACTGCTTGTGCGAAT 1719
Qy 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
Db 1720 GCCCGCGGACCGGGTGGCTATTTCACATTACACCACTAGCTGGGTGGTGGTGGTGGTGGT 1779
Qy 201 SerIleSerAlaValAlaValLeuAlaPro 210
Db 1780 TCCATTCTCGCGTTGCGGTTTATAGCCCCC 1809
RESULT 9
AAV61688
ID AAV61688 standard; DNA; 1983 BP.
XX AC AAV61688;
XX DT 03-DEC-1998 (first entry)
XX DE Hepatitis E virus hollow particle protein DNA #2.
XX KW Hollow particle protein; virus; antibody; detection; immunoassay;
XX KW infection; ss.
XX OS Hepatitis virus.
XX PN JP10234383-A.
XX PD 08-SEP-1998.
XX PF 28-FEB-1997; 97JP-00062445.
XX PR 28-FEB-1997; 97JP-00062445.
XX PA (DENK-) DENKA SEIKEN KK.
XX PA (KOKU-) KOKURITSU YOBO EISBI KENKYUSHO.
XX DR WPI; 1998-535037/46.
XX DR P-PSDB; AAW76369.
XX XX
```

PT Hepatitis E virus hollow particle poly(peptide(s) and nucleic acids
PT encoding it - useful for more accurate detection of HEV in samples, using
PT immuno-assays and nucleic acid hybridisation.

XX Claim 13; Page 24-26; 29pp; Japanese.

XX This sequence encodes a Hepatitis E viral hollow particle protein. This
CC polypeptide can be used to raise antibodies to detect HEV infection in
CC samples, e.g. by immuno-assay based techniques, and the nucleic acid can
CC be used for the same in nucleic acid hybridisation assays. The
CC polypeptides and nucleic acids allow more accurate detection of HEV than
CC previously possible

XX SQ Sequence 1983 BP; 342 A; 665 C; 485 G; 491 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,298-101 Length: 1983
Score: 1076.00 Matches: 210
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 2 Gaps: 0

US-10-089-292A-2 (1-213) x AAV61688 (1-1983)

QY 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 20
DB 1180 CAGCTGTTCTACTCCGTCCTGTCGCGCAATGGGAGCCGACTGTTAAGCTTTAT 1239
QY 21 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspLeu 40
DB 1240 ACATCTGTAGAGATGCTCAGCAGGATAAGGTATTGCAATCCCGATGACATTCACCTC 1299
QY 41 GlyGluSerArgValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
DB 1300 GGAGAATCTCGTGGTATTGAGATTATGACCAACCAACATGAAAGATCGGCGGAG 1359
QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 80
DB 1360 CTTCTCCAGCCCATCGGCCCTTCTCTGCTCCGAGCTAATGATGCTGTTGGCTC 1419
QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
DB 1420 TCTCTCACCGCTGCCGAGTATGACCATGCTTATGGCTCTTCGACTGGCCCGCTTAT 1479
QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
DB 1480 GTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGCGCGAGCCGTTGCCCGGTG 1539
QY 121 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnTyrSer 140
DB 1540 CTCGATTGGACCAAGGTACACTTGACGTCGCGCCCTCTCCACCATCCAGCAGTACTCG 1599
QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 160
DB 1600 AAGACCTCTCTTGTCTCGCGCTCCGCGTAAAGCTCTCTTCTGGGAGGACGACCAACT 1659
QY 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuValGluAsn 180
DB 1660 AAGCGGGTACCCCTTATTAATTAACACATGCTAGGACCAACTGTTGTGCGAAT 1719
QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
DB 1720 GCCCGCGGACCGCGGTGCTATTTCACCTACACCATAGCTGGTCTGCTGCTCCGTC 1779
QY 201 SerIleSerAlaValAlaValLeuAlaPro 210
DB 1780 TCCATCTCTCGCGTGTGCTGTTTATAGCCCCC 1809

RESULT 10

AAQ86592

ID AAQ86592 standard; DNA; 1984 BP.

XX

AC AAQ86592;

XX 25-MAR-2003 (revised)

XX 28-SEP-1995 (first entry)

XX Hepatitis E virus ORF2.

XX HEV; ORF2; antigen; vaccine; immunogen; ss.

XX Hepatitis E virus.

XX Key Location/Qualifiers

XX CDS 1..1983

XX /*tag= a

XX WO9508632-A1.

XX 30-MAR-1995.

XX 23-SEP-1994; 94WO-AU000572.

XX 24-SEP-1993; 93AU-00001423.

XX 15-DEC-1993; 93AU-00002964.

XX (MACF-) MACFARLANE BURNET CENT MEDICAL.

XX Anderson DA, Locarnini SA, Torresi J, Li F, Hui Z;

XX WPI; 1995-139601/18.

XX P-PSDB; AAR70323.

XX Antigen of hepatitis E virus (HEV) - selectively immuno-reactive to
PT convalescent and/or acute phase circulating antibodies to HEV.

XX Disclosure; Page 39-41; 78pp; English.

XX RNA from an HEV strain isolated in the Xinjiang region of China was
CC subjected to RT-PCR to obtain fragments corresp. to ORF2 (given in
CC AAQ86592) and ORF3 (AAQ86593) that encoded antigenic proteins (AAR70323-
CC 24, respectively). DNA fragments were manipulated into pGEX vectors for
CC production of GST fusion proteins in E. coli. Applications include HEV
CC infection diagnosis, therapy and vaccine development. (Updated on 25-MAR-
CC 2003 to correct FN field.)

XX SQ Sequence 1984 BP; 347 A; 665 C; 481 G; 490 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,298-101 Length: 1984
Score: 1076.00 Matches: 210
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 2 Gaps: 0

US-10-089-292A-2 (1-213) x AAQ86592 (1-1984)

QY 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 20
DB 1180 CAGCTGTTCTACTCCGTCCTGCTCAGCAATGGGAGCCGACTGTTAAGCTTTAT 1239
QY 21 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspLeu 40
DB 1240 ACATCTGTAGAGATGCTCAGCAGGATAAGGTATTGCAATCCCGATGACATTCACCTC 1299
QY 41 GlyGluSerArgValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
DB 1300 GGGGAGTCTCGTGTAGTATTGAGATTATGACACCAACATGACAGGACCGACGACA 1359
QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 80
DB 1360 CTTCTCCAGCCCATCGGCCCTTCTCTGCTCCGAGCTAATGATGCTGTTGGCTC 1419
QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100

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|||||
Db 1420 TCTCTACCGCTGCGAGTATGACAGTCCACTTACGGCTCTTCGACCGCCAGTCTAT 1479
Qy 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
Db 1480 GTCTCTGACTCTGTGACCTTGGTTAATGTGGACCGCGCGAGCGCTTGCCCGTCA 1539
Qy 121 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnTyrSer 140
Db 1540 CTCGACTGGACAAGGTACACACTTGTATGTCGCCCTTTCCACCATCCAGCAGTATTCA 1599
Qy 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 160
Db 1600 AAGACCTTCTTTGTCTCCGCTCCGCGTGAAGCTCTCTTTGGAGCGAGGACTACT 1659
Qy 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuValGluAsn 180
Db 1660 AAGCGCGGTACCTTTATTAATTAACACCACTGCTAGTACCAACTGCTGTGAGAA 1719
Qy 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
Db 1720 GCCGCTGGGCATCGGGTGTGCTATTTCACACTTACACCACTAGCCTGGGTGCTGCCGTC 1779
Qy 201 SerIleSerAlaValAlaValLeuAlaPro 210
Db 1780 TCTATTTCGCGGTGTGCTTTAGCCCCC 1809

RESULT 11
ABL60053
ID ABL60053 standard; DNA; 1990 BP.
XX
AC ABL60053;
XX
DT 16-AUG-2002 (first entry)
XX
DE Hepatitis E virus ORF-2 DNA #1.
XX
KW Hepatitis E virus; ORF-2; HEV; virucide; immunisation; gene; ds.
XX
OS Hepatitis E virus.
XX
PN WO200240681-A1.
XX
PD 23-MAY-2002.
XX
PF 30-SEP-2001; 2001WO-CN001459.
XX
PR 30-SEP-2000; 2000CN-00130634.
XX
PA (YANG-) YANG SHENG TANG CO LTD.
XX
PI Xia N, Zhang J, Li S, Ge S, Gu Y, He Z;
XX
WPI; 2002-427096/45.
DR
PT Polypeptide fragments of hepatitis E virus (HEV) for vaccine compositions
PT and diagnosis in preventing and treating HEV infection.
XX
PS Example 1; Page 82-83; 91pb; Chinese.
XX
CC The sequence encodes hepatitis E virus (HEV) ORF-2 polypeptide. The
CC invention relates to novel n-mer polypeptides comprising amino acids of
CC ORF-2 of HEV where n = 2-180. The polypeptides of the invention have
CC virucide activity. The polypeptide of HEV, its fragments, and chimeric
CC proteins, are useful for vaccine compositions and diagnosis in preventing
CC and treating HEV infection by immunisation, which may also be applied in
CC the diagnosis of HEV infection
XX
SQ Sequence 1990 BP; 348 A; 666 C; 481 G; 495 T; 0 U; 0 Other;
```

Alignment Scores:

Pred. No.: 3.31e-101 Length: 1990

Score: 1076.00 Matches: 210

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 6 Gaps: 0

US-10-089-292A-2 (1-213) x ABL60053 (1-1990)
Qy 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 20
Db 1180 CAGCTGTTTACTCTCGTCCGCTCTCAGCCAATGGCAGCGACTGTGTAAGCTTTAT 1239
Qy 21 ThrSerValGluAsnAlaGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 40
Db 1240 ACATCTGTAGAGATGCTCAGCAGATGAAGGTATTGCAATCCCGCATGACATCCACTC 1299
Qy 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
Db 1300 GGGGAGTCTCGTGTAGTTATTTCAGGATTTATGCAACCAACATGAGCAGACCGACGA 1359
Qy 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 80
Db 1360 CTTTCCCGCAGCCCATCGCGCTTTTCTGTCTCCGAGCTAATGATGTGCTTTGGCTT 1419
Qy 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
Db 1420 TCTCTCACCGCTCGCGAGTATGACCACTTACGGCTCTTCGACCGGCCAGTCTAT 1479
Qy 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
Db 1480 GTCTCTGACTCTGTGACCTTGGTTAATGTTCGACCGCGCGAGCGCTTGCCCGTCA 1539
Qy 121 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnTyrSer 140
Db 1540 CTCGACTGGACAAGGTACACACTTGTATGTCGCCCTTTCCACCATCCAGCAGTATTCA 1599
Qy 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 160
Db 1600 AAGACCTTCTTTGTCTCCGCTCCGCGTGAAGCTCTCTTTGGAGCGAGGACTACT 1659
Qy 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuValGluAsn 180
Db 1660 AAGCGCGGTACCTTTATTAATTAACACCACTGCTAGTACCAACTGCTGTGAGAA 1719
Qy 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
Db 1720 GCCGCTGGGCATCGGGTGTGCTATTTCACACTTACACCACTAGCCTGGGTGCTGCCGTC 1779
Qy 201 SerIleSerAlaValAlaValLeuAlaPro 210
Db 1780 TCTATTTCGCGGTGTGCTTTAGCCCCC 1809

RESULT 12
ADB97808
ID ADB97808 standard; DNA; 1990 BP.
XX
AC ADB97808;
XX
DT 04-DEC-2003 (first entry)
XX
DE HEV ORF2 DNA #SEQ ID 2.
XX
KW Hepatitis E virus; HEV; virucide; vaccine; monoclonal antibody; NE2;
KW infection; ds.
XX
OS Hepatitis E virus.
XX
PN WO2003040187-A1.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002WO-CN000797.
XX
PR 08-NOV-2001; 2001CN-00134643.
```

XX (YANG-) YANG SHENG TANG CO LTD.
XX Xia N, Zhang J, Gu Y, Li S, Ge S, He Z;
XX WPI; 2003-441530/41.
XX Hepatitis E virus monoclonal antibodies and their active fragments, for
XX use in diagnosis and developing remedies e.g. vaccines for preventing or
XX treating hepatitis E virus infection.
XX Example 1; Page 131-133; 165pp; Chinese.
XX The invention relates to a monoclonal antibody that binds specifically to
XX hepatitis E virus open-reading frame (ORF) 2. Also disclosed are
XX nucleotide sequences encoding the heavy-chain and/or light-chain variable
XX region of their degeneration sequences. The monoclonal antibody is
XX selected from anti-HEV monoclonal antibody 8C11 secreted by hybridoma
XX C2C-C200116, anti-HEV monoclonal antibody 13D8 secreted by hybridoma
XX C2C-C200114, anti-HEV monoclonal antibody 8H3 secreted by hybridoma
XX C2C-C200117, and anti-HEV monoclonal antibody 16D7 secreted by
XX hybridoma C2C-C200114. The monoclonal antibodies and their active
XX fragments are useful in diagnosis and developing remedies e.g. vaccines
XX for preventing or treating hepatitis E virus infection. From the whole
XX HEV gene obtained in patients, the HEV ORF fragment was prepared by using
XX the method of Aye et al. The polypeptide NE2 was then expressed and
XX isolated after biotechnological manipulations, which was characterised.
XX Its analogs were also produced for immunising mice and construction of
XX hybridomas. Tests were carried out to confirm usefulness of such
XX polypeptides and monoclonal antibodies. The current sequence represents
XX the HEV ORF2 encoding DNA.
XX Sequence 1990 BP; 348 A; 666 C; 481 G; 495 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 3,31e-101 Length: 1990
Score: 1076.00 Matches: 210
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 10 Gaps: 0

US-10-089-292A-2 (1-213) x ADB97808 (1-1990)

QY 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 20
DB 1180 CAGCTGTTTACTCTCTGTCCTCCGTCGTCAGCCAAATGGCGAGCGACTGTAACTTTAT 1239

QY 21 ThrSerValGluAsnAlaGlnAspLysGlyIleAlaIleProHisAspLeu 40
DB 1240 ACATCTGTAGAGAAATGCTCAGCAGGATAAGGGTATTGCAATCCGCATGCACATCGACCTC 1299

QY 41 GlyLysSerArgValValIleGlnAspTyrAspAsnGlnHisGluClnAspArgProThr 60
DB 1300 GGGAGTCTCGTGTAGTTATTCAGGATTATGACAAACATGAGCAGACCGACCGACA 1359

QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 80
DB 1360 CCTTCCCGAGCCCATCGCGCCCTTTCTGTCTCGAGCTAAATGATGTGCTTGGCTT 1419

QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
DB 1420 TCTCTCACCGCTCCGAGTATGACCATGTCACATTCAGGCTCTTCGACCGCGCCGCTAT 1479

QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyValGlnAlaValAlaArgSer 120
DB 1480 GTCTCTGACTCTGTGACCTTGGTTATGTTCACCGCGCGCGAGCCGTTGCCCGGTCA 1539

QY 121 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnIntyrSer 140
DB 1540 CTCGACTGGACCAAGGTCACTCATGTTGTCGCGCCCTTTCCACCATCCAGCAGTATTCA 1599

QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 160

DB 1600 AAGACCTTCTTTGTCTCCCGCTCGCGGTAAAGTCTCTCTTTTGGGAGGCGAGGTACTACT 1659

QY 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuValGluAsn 180
DB 1660 AAGCCGGGTACCCCTTAAATTAATAACCACTGCTAGTACCACTGCTCTGTGAGAT 1719

QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
DB 1720 GCGCTGGGCATCGGTTGCTATTTCACCTACACCACTAGCTGGGTGGTGGTCCCGTC 1779

QY 201 SerIleSerAlaValAlaValLeuAlaPro 210
DB 1780 TCTATTTCGCGGTGCTGTTTGTAGCCCC 1809

RESULT 13
AAT27107
ID AAT27107 standard; DNA; 2049 BP.
XX
AC AAT27107;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
DE Hepatitis E virus (Burma strain) ORF-2.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid; ds.
XX
OS Hepatitis E virus; Burma strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbrough PO, Zhang Y;
XX
DR WPI; 1996-230608/23.
XX
PS P-PSDB; AAR96089.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
XX diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Disclosure; Page 69-70; 125pp; English.
XX
CC The hepatitis E virus (HEV) Burma strain ORF-2 (AAT27107) codes for the
XX putative capsid protein (AAR96089). PCR amplification of ORF-2 allows
XX prodn. of capsid protein or of C-terminal regions of the capsid protein
XX (see also AAR96091, AAR96093 and AAR96095) and expression in Spodoptera
XX frugiperda Sf9 insect cells using a baculovirus vector provides
XX recombinant C-terminal regions (see also AAR96101 and AAR96103) useful as
XX diagnostic reagents and in vaccines. The HEV Mexico strain ORF-2
XX (AAT27108) may similarly be used. (Updated on 16-OCT-2003 to standardise
XX OS field)
XX
SQ Sequence 2049 BP; 344 A; 686 C; 496 G; 523 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,44e-101 Length: 2049
Score: 1076.00 Matches: 210
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 2 Gaps: 0

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US-10-089-292A-2 (1-213) x ANT27107 (1-2049)
QY 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValIysLeuTyr 20
DB 1180 CAGCTGTTCTACTCCCGTCCCGTGTCTCAGCAATGGCGAGCCGACTGTTAAGTTGAT 1239
QY 21 ThrSerValGluAsnAlaGlnAspIysGlyIleAlaIleProHisAspIleAspLeu 40
DB 1240 ACATCTGTAGAGAAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGCATTCACCTC 1299
QY 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
DB 1300 GGAGAAATCTCGTGTGTTATTACAGATTATGATATACCAACATGACAAAGATCGGCCGAG 1359
QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 80
DB 1360 CCTTCTCCAGCCCATCGCCCTTCTCTGTCCTTCGAGCTAATGATGCTTTGGCTC 1419
QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
DB 1420 TCTCTCACCGCTGCCGAGTATGACAGTCCACTTATGGCTCTTCGACTGGCCAGTTTAT 1479
QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyValAlaGlnAlaValAlaArgSer 120
DB 1480 GTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGCGCGCAGCGCTGTCGCCGTCG 1539
QY 121 LeuAspTTPThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnIleNTrpSer 140
DB 1540 CTCGATTGGACCAAGGTACACTTCAGCGTCCGCCCTCTCCACCATCCAGCAGTACTCG 1599
QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 160
DB 1600 AAGACCTCTTCTGCTCCGCTCCGCGGTAAAGCTCTCTTTCTGGAGGCGAGGCAACT 1659
QY 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuValGluAsn 180
DB 1660 AAAGCGGGTACCTTTAATTAATTAACCACTGCTAGGACCAACTGCTGTGTCAGAAAT 1719
QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
DB 1720 GCCGCGGGGACCGGGTCCGCTATTTCACCTTACACCACTAGGCTGGGTGCTGGTCCGCTC 1779
QY 201 SerIleSerAlaValAlaValLeuAlaPro 210
DB 1780 TCCATTTCGCGGTGCGGTTTTAGCCCCC 1809
RESULT 14
AAS01448
ID AAS01448 standard; cDNA; 2054 BP.
AC
XX
AC AAS01448;
XX
XX 11-SEP-2003 (revised)
DT 18-JUL-2001 (first entry)
XX
DE Hepatitis E virus (HEV) ORF2 cDNA.
XX
XX Hepatitis E virus; HEV; E2; pE2; ORF2; immunoreactive viral peptide;
KW antigenic activity; viral infection; ss.
XX
OS Hepatitis E virus; Chinese strain D11092.
XX
XX Key Location/Qualifiers
FH 1. .1983
CDS /tag= a
FT /product= "Major HEV structural protein"
FT 1180. .1990
FT /tag= b
FT /note= "Corresponds to residues 1-810 of E2"
FT mutation replace(1810. .1812, CC)
FT /tag= c
FT /note= "Single base deletion present in E2"
XX
```

PN WO200122916-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-IB0011393.
XX
PR 30-SEP-1999; 99CA-02283538.
XX
PA (UYHK-) UNIV HONG KONG.
XX
PI Ng MH, Im S, Zhang J;
XX WPI; 2001-266109/27.
XX
PT New immunoreactive peptide pE2, cloned from the genome of a Chinese
PT strain of hepatitis E virus (HEV), for detecting and diagnosing HEV
PT infection and for use as a vaccine for prevention of the viral infection
PT in humans.
XX
PS Disclosure; Fig 2A-2D; 101pp; English.
XX
CC The present sequence for hepatitis E virus (HEV) ORF2 cDNA is used to
CC clone a cDNA fragment E2 (AAS01434) which encodes for a novel peptide,
CC pE2. During the cloning of the E2 fragment a single base deletion
CC (presumed to be a PCR amplification error) at position 1811 of ORF2
CC resulted in a frame shift causing the premature termination at a new stop
CC codon at position 1820-1822, and giving rise to a smaller peptide, pE2.
CC Peptide pE2 is a highly immunoreactive viral peptide which can be used in
CC the development of diagnostic methods for the detection of HEV. Peptide
CC pE2 which has antigenic activity is also useful as a vaccine for
CC immunising an individual against infection from HEV and for determining
CC the presence of HEV antibodies in a biological test sample such as human
CC blood serum or plasma for detection and diagnosis of HEV infection. An
CC antibody against pE2 is useful for detecting an HEV particle, in a
CC biological test sample. The use of recombinant peptides such as pE2
CC peptide have advantage over the prior art of using live intact virus
CC particles by avoiding the potential risk of infectivity. The ORF3
CC (AAS01449) of HEV Chinese strain D11092 is used to clone a cDNA fragment
CC E3 (AAS01450) which encodes pE3 peptide. (Updated on 11-SEP-2003 to
CC standardise OS field)
XX
SQ Sequence 2054 BP; 355 A; 687 C; 491 G; 521 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.45e-101 Length: 2054
Score: 1076.00 Matches: 210
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 4 Gaps: 0

US-10-089-292A-2 (1-213) x AAS01448 (1-2054)
QY 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValIysLeuTyr 20
DB 1180 CAGCTGTTCTACTCCCGTCCCGTGTCTCAGCAATGGCGAGCCGACTGTTAAGTTTAT 1239
QY 21 ThrSerValGluAsnAlaGlnAspIysGlyIleAlaIleProHisAspIleAspLeu 40
DB 1240 ACATCTGTAGAGAAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGCATTCACCTC 1299
QY 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
DB 1300 GGCGAGTCTCGTGTAGTTATTTCAGGATTATGACAACTATGACAGCAGCCGACGACA 1359
QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 80
DB 1360 CTTTCCCGAGCCCATCGGCCCTTTTCTGCTCCCGAGCTAATGATGCTTTGGCTT 1419
QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
DB 1420 TCTCTCACCGCTGCCGAGTATGACAGTCCACTTACGGCTCTTCAGGCTCTTCAGCCGCCGCTCTAT 1479

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QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
Db 1480 GTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGCGCGAGCGGTTGCCCGGTCA 1539
QY 121 LeuAspThrThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
Db 1540 CTCGACTGACCAAGGTACACTTGTATGTCGCCCTTTCCACCATCCAGCAGTATTCA 1599
QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTyrGluAlaGlyThrThr 160
Db 1600 AAGACTTCTTTTGTCTGCGCGTCCGCGTAGACTCTCTTTTGGAGCAGGTACTACT 1659
QY 161 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuValGluAsn 180
Db 1660 AAAGCCGGTACCTTATAATTAACACCACTGCTAGTACCAACTGCTGCTGTTGAGAAT 1719
QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
Db 1720 GCCGCTGGGCATCGGGTTGCTATTTCCTTACACCACTAGCTGGGTGCTGGTCCCGTC 1779
QY 201 SerIleSerAlaValAlaValLeuAlaPro 210
Db 1780 TCTATTTCGCGGTGCTGTTTAGCCCCC 1809
RESULT 15
ID AAQ47129 standard; DNA; 2094 BP.
XX AC AAQ47129;
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 11-JAN-1994 (first entry)
DE HEV third and second ORFs.
XX KW Enterically transmitted non-A non-B hepatitis; ET-NANB; vaccine; ss.
XX OS Hepatitis E virus; Burma strain.
XX FH Key
FT CDS 5..376 Location/Qualifiers
FT FT /*tag= a'
FT FT /label= ORF3
FT CDS 46..2094
FT FT /*tag= b
FT FT /label= ORF2
FT misc_RNA 275..376
FT FT /*tag= c
FT FT /label= 406.4-2
FT FT 718..2029
FT FT /*tag= d
FT FT /label= C2
FT FT 1045..2029
FT FT /*tag= e
FT FT /label= SG3
FT FT 1882..2029
FT FT /*tag= f
FT FT /label= 406.3-2
XX WO9314116-AL.
XX 22-JUL-1993.
XX 15-JAN-1993; 93WO-US000459.
XX 17-JAN-1992; 92US-00822335.
PR 01-MAY-1992; 92US-00876941.
XX (GENE-) GENELABS TECHNOLOGIES INC.
PA (USSH ) US SEC DEPT HEALTH.
XX Reyes GR, Bradley DW, Tam AW, Carl M;
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XX WPI; 1993-243144/30.
DR P-PSDB; AAR38784, AAR38785.
XX New immunogenic hepatitis E virus (HEV) peptide(s) - are from the ORF1,
PT ORF2 and ORF3 regions of HEV, useful as a vaccine against HEV infection.
XX Disclosure; Fig 7; 48pp; English.
XX Immunogenic hepatitis E virus (HEV) peptides are selected from the ORF1,
CC ORF2 and ORF3 regions of HEV. The peptides can be used in vaccines to
CC prevent infection by HEV. The antibodies can neutralise and block HEV
CC infection and can be used to prevent or treat HEV infection. The peptides
CC and antibodies can also be used as diagnostic reagents. (Updated on 25-
CC MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS
CC field)
XX Sequence 2094 BP; 353 A; 697 C; 508 G; 536 T; 0 U; 0 Other;
SQ Alignment Scores:
Pred. No.: 3.54e-101 Length: 2094
Score: 1076.00 Matches: 210
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 2 Gaps: 0
US-10-089-292A-2 (1-213) x AAQ47129 (1-2094)
QY 1 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 20
Db 1225 CAGCTGTTCTACTCCCGTCCGTTGTCTCAGCAATGGCGAGCCGACTGTTAAGTTGAT 1284
QY 21 ThrSerValGluAsnAlaGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 40
Db 1285 ACATCTGTAGAGATGCTCAGCAGGATAAGGTTATGCAATCCCGCATGACATTGACCTC 1344
QY 41 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 60
Db 1345 GGAGAATCTCGTGTGTTATTTCAGGATTTATGATACCAACATGAACAGATCGGCCGAG 1404
QY 61 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTyrLeu 80
Db 1405 CCTTCTCCAGCCCCATCGGCCCTTCTCTGCTTCGAGCTAATGATGTGTTGGCTC 1464
QY 81 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 100
Db 1465 TCTCTCACCGCTGCCGAGTATGACCACTTATGCTCTTCGACTGGCCAGTTTAT 1524
QY 101 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 120
Db 1525 GTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGCGCGCGCGTTCGCCGGTGC 1584
QY 121 LeuAspThrThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 140
Db 1585 CTCGATTGGACCAAGGTACACTTGACGTCGCCCTCTCCACCATCCAGCAGTACTCG 1644
QY 141 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTyrPduAlaGlyThrThr 160
Db 1645 AAGACTTCTTGTCTTCGCCGCTCCGCGTAAAGTCTCTTTCTGGGAGGAGGACCAACT 1704
QY 161 LysAlaGlyTyrProTyrAsnThrThrAlaSerAspGlnLeuValGluAsn 180
Db 1705 AAAGCCGGTACCTTATAATTAACACCACTGTAGCAGCAACTGCTGTCAGAAAT 1764
QY 181 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 200
Db 1765 GCCGCGGGCACCGGGTCCGTAATTTCCACTTACACCACTAGCTGGGTGCTGTCCTCCGTC 1824
QY 201 SerIleSerAlaValAlaValLeuAlaPro 210
Db 1825 TCCATTCTCGGTTGCCGTTTTCGTTTAGCCCCC 1854
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